

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Keeling, Peter
Guan, Hanping

(ii) TITLE OF INVENTION: Starch Encapsulation

(iii) NUMBER OF SEQUENCES: 37

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
- (B) STREET: 5370 Manhattan Circle
- (C) CITY: Boulder
- (D) STATE: CO
- (E) COUNTRY: US
- (F) ZIP: 80303

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US
- (B) FILING DATE: 30-SEP-1997
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 60/026,855
- (B) FILING DATE: 30-SEP-1996

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Winner, Ellen P
- (B) REGISTRATION NUMBER: 28,547
- (C) REFERENCE/DOCKET NUMBER: 89-97

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (303) 499-8080
- (B) TELEFAX: (303) 499-8089

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Oligonucleotide"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GACTAGTCAT ATGGTGAGCA AGGGCGAGGA G

31

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Oligonucleotide"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTAGATCTTC ATATGTTGT ACAGCTCGTC CATGCC

36

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTAGATCTTG GCCATGGCCT TGTACAGCTC GTCCATGCC

39

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4800 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Zea mays

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(1449..1553, 1685..1765, 1860..1958, 2055 ..2144, 2226..2289, 2413..2513, 2651..2760, 2858 ..3101, 3212..3394, 3490..3681, 3793..3879, 3977 ..4105, 4227..4343)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAGCGACCTA TTACACAGCC CGCTCGGGCC CGCGACGTGCG GGACACATCT TCTTCCCCCT

60

TTTGGTGAAG CTCTGCTCGC AGCTGTCCGG CTCCCTGGAC GTTCGTGTGG CAGATTCACTC

120

TGTTGTCTCG TCTCCTGTGC TTCCTGGTA GCTTGTGTAG TGGAGCTGAC ATGGTCTGAG

180

CAGGCTTAAA ATTTGCTCGT AGACGAGGAG TACCAGCACA GCACGTTGCG GATTCTCTG

240

CCTGTGAAGT GCAACGTCTA GGATTGTCAC ACGCCTTGGT CGCGTCGCGT CGCGTCGCGT	300		
CGATGCGGTG GTGAGCAGAG CAGCAACAGC TGGGCGGCC AACGTTGGCT TCCGTGTCTT	360		
CGTCGTACGT ACGCGCGCC CGGGGACACG CAGCAGAGAG CGGAGAGCGA GCCGTGCACG	420		
GGGAGGTGGT GTGGAAGTGG AGCCGCGCGC CGGGCCGCC GCGCCCGGTG GGCAACCAA	480		
AAGTACCCAC GACAAGCGAA GGCGCCAAAG CGATCCAAGC TCCGGAACGC AACAGCATGC	540		
GTCGCGTCGG AGAGCCAGCC ACAAGCAGCC GAGAACCGAA CCGGTGGCG ACAGCTCATG	600		
GGACGGACGC GGGCGACGCT TCCAAACGGG CCACGTACGC CGGCGTGTGC GTGCGTGCAG	660		
ACGACAAGCC AAGGCGAGGC AGCCCCGAT CGGGAAAGCG TTTTGGCGC GAGCGCTGGC	720		
GTGCGGGTCA GTCGCTGGTG CGCAGTGCCG GGGGAACGG GTATCGTGGG GGGCGCGGC	780		
GGAGGAGAGC GTGGCGAGGG CCGAGAGCAG CGCGCGGCCG GGTACCGCAA CGCGCCCCAC	840		
GTACTGCCCT CCCCCCTCCGC GCGCGCTAGA AATACCGAGG CCTGGACCAGG GGGGGGGCCC	900		
CGTCACATCC ATCCATCGAC CGATCGATCG CCACAGCCAA CACCACCCGC CGAGGCGACG	960		
CGACAGCCGC CAGGAGGAAG GAATAAACTC ACTGCCAGCC AGTGAAGGGG GAGAAGTGT	1020		
CTGCTCCGTC GACCAAGTGGC CGCACCGCCC GGCAGGGCTG CTCATCTCGT CGACGACCAG	1080		
GTTCTGTTCC GTTCCGATCC GATCCGATCC TGTCTTGAG TTTCGTCCAG ATCCTGGCGC	1140		
GTATCTCGGT GTTTGATGAT CCAGGTTCTT CGAACCTAAA TCTGTCCGTG CACACGTCTT	1200		
TTCTCTCTCT CCTACGCAGT GGATTAATCG GCATGGCGGC TCTGCCACG TCGCAGCTCG	1260		
TCGCAACGCG CGCCGGCCTG GGCGTCCCGG ACGCGTCCAC GTTCCGCCGC GGCGCCGCGC	1320		
AGGGCCTGAG GGGGGCCCGG GCGTCGGCGG CGCGGGACAC GTCAGCATG CGGACCAGCG	1380		
CGCGCGCGGC GCCCAGGCAC CAGCAGCAGG CGCGCCGCGG GGGCAGGTTG CCGTCGCTCG	1440		
TCGTGTGC GCC AGC GCC GGC ATG AAC GTC GTC TTC GTC GGC GCC GAG ATG Ala Ser Ala Gly Met Asn Val Val Phe Val Gly Ala Glu Met	1490		
1	5	10	
GCG CCG TGG AGC AAG ACC GGC GGC CTC GGC GAC GTC CTC GGC GGC CTG	1538		

Ala Pro Trp Ser Lys Thr Gly Gly Leu Gly Asp Val Leu Gly Gly Leu				
15	20	25	30	
CCG CCG GCC ATG GCC GTAAGCGCGC GCACCGAGAC ATGCATCCGT TGGATCGCGT				1593
Pro Pro Ala Met Ala				
35				
CTTCTTCGTG CTCTTGCCGC GTGCATGATG CATGTGTTTC CTCCTGGCTT GTGTTCGTGT				1653
ATGTGACGTG TTTGTTCGGG CATGCATGCA G GCG AAC GGG CAC CGT GTC ATG				1705
Ala Asn Gly His Arg Val Met				
40				
GTC GTC TCT CCC CGC TAC GAC CAG TAC AAG GAC GCC TGG GAC ACC AGC				1753
Val Val Ser Pro Arg Tyr Asp Gln Tyr Lys Asp Ala Trp Asp Thr Ser				
45	50	55		
GTC GTG TCC GAG GTACGGCCAC CGAGACCAGA TTCAGATCAC AGTCACACAC				1805
Val Val Ser Glu				
60				
ACCGTCATAT GAACTTTCT CTGCTCTGAT GCCTGCAACT GCAAATGCAT GCAG ATC				1862
Val	Ile			
AAG ATG GGA GAC GGG TAC GAG ACG GTC AGG TTC TTC CAC TGC TAC AAG				1910
Lys Met Gly Asp Gly Tyr Glu Thr Val Arg Phe Phe His Cys Tyr Lys				
65	70	75		
CGC GGA GTG GAC CGC GTG TTC GTT GAC CAC CCA CTG TTC CTG GAG AGG				1958
Arg Gly Val Asp Arg Val Phe Val Asp His Pro Leu Phe Leu Glu Arg				
80	85	90	95	
GTGAGACGAG ATCTGATCAC TCGATAACGCA ATTACCACCC CATTGTAAGC AGTTACAGTG				2018
AGCTTTTTT CCCCCCGGCC TGGTCGCTGG TTTCAG GTT TGG GGA AAG ACC GAG				2072
Val Trp Gly Lys Thr Glu				
100				
GAG AAG ATC TAC GGG CCT GTC GCT GGA ACG GAC TAC AGG GAC AAC CAG				2120
Glu Lys Ile Tyr Gly Pro Val Ala Gly Thr Asp Tyr Arg Asp Asn Gln				
105	110	115		
CTG CGG TTC AGC CTG CTA TGC CAG GTCAGGATGG CTTGGTACTA CAACTTCATA				2174
Leu Arg Phe Ser Leu Leu Cys Gln				

120	125	
TCATCTGTAT GCAGCAGTAT ACACTGATGA GAAATGCATG CTGTTCTGCA G GCA GCA		
		2231
Ala Ala		
CTT GAA GCT CCA AGG ATC CTG AGC CTC AAC AAC AAC CCA TAC TTC TCC		
Leu Glu Ala Pro Arg Ile Leu Ser Leu Asn Asn Asn Pro Tyr Phe Ser		
130	135	140
GGA CCA TAC G GTAAGAGTTG CAGTCTTCGT ATATATATCT GTTGAGCTCG		
Gly Pro Tyr		
145		
AGAATCTTCA CAGGAAGCGG CCCATCAGAC GGACTGTCAT TTTACACTGA CTACTGCTGC		
TGCTCTTCGT CCATCCATAC AAG GG GAG GAC GTC GTG TTC GTC TGC AAC		
Gly Glu Asp Val Val Phe Val Cys Asn		
150	155	
GAC TGG CAC ACC GGC CCT CTC TCG TGC TAC CTC AAG AGC AAC TAC CAG		
Asp Trp His Thr Gly Pro Leu Ser Cys Tyr Leu Lys Ser Asn Tyr Gln		
160	165	170
TCC CAC GGC ATC TAC AGG GAC GCA AAG GTTGCCTTCT CTGAAGTGAA		
Ser His Gly Ile Tyr Arg Asp Ala Lys		
175	180	
CAACGCCGTT TTCTGTTCTCC ATGCTCGTAT ATACCTCGTC TGGTAGTGGT GGTGCTTCTC		
TGAGAAACTA ACTGAAACTG ACTGCATGTC TGTCTGACCA TCTTCACGTA CTACCAG		
ACC GCT TTC TGC ATC CAC AAC ATC TCC TAC CAG GGC CGG TTC GCC TTC		
Thr Ala Phe Cys Ile His Asn Ile Ser Tyr Gln Gly Arg Phe Ala Phe		
185	190	195
TCC GAC TAC CCG GAG CTG AAC CTC CCG GAG AGA TTC AAG TCG TCC TTC		
Ser Asp Tyr Pro Glu Leu Asn Leu Pro Glu Arg Phe Lys Ser Ser Phe		
200	205	210
GAT TTC ATC GAC GG GTCTGTTTC CTGCGTGCAT GTGAACATTC ATGAATGGTA		
Asp Phe Ile Asp Gly		
215		
ACCCACAAC GTTCGGGTCC TGCTGGTTCA TTATCTGACC TGATTGCATT ATTGCAG C		
2858		

TAC GAG AAG CCC GTG GAA GGC CGG AAG ATC AAC TGG ATG AAG GCC GGG		2906
Tyr Glu Lys Pro Val Glu Gly Arg Lys Ile Asn Trp Met Lys Ala Gly		
220	225	230
ATC CTC GAG GCC GAC AGG GTC CTC ACC GTC AGC CCC TAC TAC GCC GAG		2954
Ile Leu Glu Ala Asp Arg Val Leu Thr Val Ser Pro Tyr Tyr Ala Glu		
235	240	245
GAG CTC ATC TCC GGC ATC GCC AGG GGC TGC GAG CTC GAC AAC ATC ATG		3002
Glu Leu Ile Ser Gly Ile Ala Arg Gly Cys Glu Leu Asp Asn Ile Met		
250	255	260
CGC CTC ACC GGC ATC ACC GGC ATC GTC AAC GGC ATG GAC GTC AGC GAG		3050
Arg Leu Thr Gly Ile Thr Gly Ile Val Asn Gly Met Asp Val Ser Glu		
270	275	280
TGG GAC CCC AGC AGG GAC AAG TAC ATC GCC GTG AAG TAC GAC GTG TCG		3098
Trp Asp Pro Ser Arg Asp Lys Tyr Ile Ala Val Lys Tyr Asp Val Ser		
285	290	295
ACG GTGAGCTGGC TAGCTCTGAT TCTGCTGCCT GGTCCCTCCTG CTCATCATGC		3151
Thr		
TGGTTCGGTA CTGACGCGGC AAGTGTACGT ACGTGCGTGC GACGGTGGTG TCCGGTTCA		3211
GCC GTG GAG GCC AAG GCG CTG AAC AAG GAG GCG CTG CAG GCG GAG GTC		3259
Ala Val Glu Ala Lys Ala Leu Asn Lys Glu Ala Leu Gln Ala Glu Val		
300	305	310
GGG CTC CCG GTG GAC CGG AAC ATC CCG CTG GTG GCG TTC ATC GGC AGG		3307
Gly Leu Pro Val Asp Arg Asn Ile Pro Leu Val Ala Phe Ile Gly Arg		
315	320	325
CTG GAA GAG CAG AAG GGC CCC GAC GTC ATG GCG GCC GCG ATC CCG CAG		3355
Leu Glu Glu Gln Lys Gly Pro Asp Val Met Ala Ala Ala Ile Pro Gln		
335	340	345
CTC ATG GAG ATG GTG GAG GAC GTG CAG ATC GTT CTG CTG GTACGTGTGC		3404
Leu Met Glu Met Val Glu Asp Val Gln Ile Val Leu Leu		
350	355	
GCCGGCCGCC ACCCGGCTAC TACATGCGTG TATCGTTCGT TCTACTGGAA CATGCGTGTG		3464
AGCAACGCGA TGGATAATGC TGCAG GGC ACG GGC AAG AAG AAG TTC GAG CGC		3516

Gly Thr Gly Lys Lys Lys Phe Glu Arg 360 365		
ATG CTC ATG AGC GCC GAG GAG AAG TTC CCA GGC AAG GTG CGC GCC GTG Met Leu Met Ser Ala Glu Glu Lys Phe Pro Gly Lys Val Arg Ala Val 370 375 380		3564
GTC AAG TTC AAC GCG GCG CTG GCG CAC CAC ATC ATG GCC GGC GCC GAC Val Lys Phe Asn Ala Ala Leu Ala His His Ile Met Ala Gly Ala Asp 385 390 395 400		3612
GTG CTC GCC GTC ACC AGC CGC TTC GAG CCC TGC GGC CTC ATC CAG CTG Val Leu Ala Val Thr Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln Leu 405 410 415		3660
CAG GGG ATG CGA TAC GGA ACG GTACGAGAGA AAAAAAAAAT CCTGAATCCT Gln Gly Met Arg Tyr Gly Thr 420		3711
GACGAGAGGG ACAGAGACAG ATTATGAATG CTTCATCGAT TTGAATTGAT TGATCGATGT		3771
CTCCCGCTGC GACTCTTGCA G CCC TGC GCC TGC GCG TCC ACC GGT GGA CTC Pro Cys Ala Cys Ala Ser Thr Gly Gly Leu 425 430		3822
GTC GAC ACC ATC ATC GAA GGC AAG ACC GGG TTC CAC ATG GCC CGC CTC Val Asp Thr Ile Ile Glu Gly Lys Thr Gly Phe His Met Gly Arg Leu 435 440 445		3870
AGC GTC GAC GTAAGCCTAG CTCTGCCATG TTCTTTCTTC TTTCTTCTG Ser Val Asp 450		3919
TATGTATGTA TGAATCAGCA CCGCCGTTCT TGTTTCGTCG TCGTCCTCTC TTCCCAG		3976
TGT AAC GTC GTG GAG CCG GCG GAC GTC AAG AAG GTG GCC ACC ACA TTG Cys Asn Val Val Glu Pro Ala Asp Val Lys Lys Val Ala Thr Thr Leu 455 460 465		4024
CAG CGC GCC ATC AAG GTG GTC GGC ACG CCG GCG TAC GAG GAG ATG GTG Gln Arg Ala Ile Lys Val Val Gly Thr Pro Ala Tyr Glu Glu Met Val 470 475 480		4072
AGG AAC TGC ATG ATC CAG GAT CTC TCC TGG AAG GTACGTACGC CCGCCCCGCC Arg Asn Cys Met Ile Gln Asp Leu Ser Trp Lys		4125

485	490	495	
CCGGCCCCGCC AGAGCAGAGC GCCAAGATCG ACCGATCGAC CGACCACACG TACGCGCCTC			4185
GCTCCTGTGCG CTGACCGTGG TTTAATTGCA G GGC CCT GCC AAG Gly Pro Ala Lys			4238
AAC TGG GAG AAC GTG CTG CTC AGC CTC GGG GTC GCC GGC GGC GAG CCA Asn Trp Glu Asn Val Leu Leu Ser Leu Gly Val Ala Gly Gly Glu Pro			4286
500	505	510	515
GGG GTC GAA GGC GAG GAG ATC GCG CCG CTC GCC AAG GAG AAC GTG GCC Gly Val Glu Gly Glu Ile Ala Pro Leu Ala Lys Glu Asn Val Ala			4334
520	525	530	
GCG CCC TGA AGAGTTCGGC CTGCAGGGCC CCTGATCTCG CGCGTGGTGC Ala Pro *			4383
AAAGATGTTG GGACATCTTC TTATATATGC TGTTTCGTTT ATGTGATATG GACAAGTATG			4443
TGTAGCTGCT TGCTTGTGCT AGTGTAAATGT AGTGTAGTGG TGGCCAGTGG CACAACCTAA			4503
TAAGCCCATG AACTAATTGC TTGCGTGTGT AGTTAAGTAC CGATCGGTAA TTTTATATTG			4563
CGAGTAAATA AATGGACCTG TAGTGGTGGA GTAAATAATC CCTGCTGTTG GGTGTTCTTA			4623
TCGCTCCTCG TATAGATATT ATATAGAGTA CATTTCCTC TCTCTGAATC CTACGTTGT			4683
GAAATTCTA TATCATTACT GTAAAATTTC TGCGTTCCAA AAGAGACCAC AGCCTATCTT			4743
TGGCCCTGTT TGTTTCGGCT TCTGGCAGCT TCTGGCCACC AAAAGCTGCT GCGGACT			4800

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 534 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ala Ser Ala Gly Met Asn Val Val Phe Val Gly Ala Glu Met Ala Pro
 1 5 10 15

Trp Ser Lys Thr Gly Gly Leu Gly Asp Val Leu Gly Gly Leu Pro Pro
 20 25 30

Ala Met Ala Ala Asn Gly His Arg Val Met Val Val Ser Pro Arg Tyr
 35 40 45

Asp Gln Tyr Lys Asp Ala Trp Asp Thr Ser Val Val Ser Glu Ile Lys
 50 55 60

Met Gly Asp Gly Tyr Glu Thr Val Arg Phe Phe His Cys Tyr Lys Arg
 65 70 75 80

Gly Val Asp Arg Val Phe Val Asp His Pro Leu Phe Leu Glu Arg Val
 85 90 95

Trp Gly Lys Thr Glu Glu Lys Ile Tyr Gly Pro Val Ala Gly Thr Asp
 100 105 110

Tyr Arg Asp Asn Gln Leu Arg Phe Ser Leu Leu Cys Gln Ala Ala Leu
 115 120 125

Glu Ala Pro Arg Ile Leu Ser Leu Asn Asn Asn Pro Tyr Phe Ser Gly
 130 135 140

Pro Tyr Gly Glu Asp Val Val Phe Val Cys Asn Asp Trp His Thr Gly
 145 150 155 160

Pro Leu Ser Cys Tyr Leu Lys Ser Asn Tyr Gln Ser His Gly Ile Tyr
 165 170 175

Arg Asp Ala Lys Thr Ala Phe Cys Ile His Asn Ile Ser Tyr Gln Gly
 180 185 190

Arg Phe Ala Phe Ser Asp Tyr Pro Glu Leu Asn Leu Pro Glu Arg Phe
 195 200 205

Lys Ser Ser Phe Asp Phe Ile Asp Gly Tyr Glu Lys Pro Val Glu Gly
 210 215 220

Arg Lys Ile Asn Trp Met Lys Ala Gly Ile Leu Glu Ala Asp Arg Val
 225 230 235 240

Leu Thr Val Ser Pro Tyr Tyr Ala Glu Glu Leu Ile Ser Gly Ile Ala
 245 250 255

Arg Gly Cys Glu Leu Asp Asn Ile Met Arg Leu Thr Gly Ile Thr Gly
 260 265 270

Ile Val Asn Gly Met Asp Val Ser Glu Trp Asp Pro Ser Arg Asp Lys
 275 280 285

Tyr Ile Ala Val Lys Tyr Asp Val Ser Thr Ala Val Glu Ala Lys Ala
 290 295 300

Leu Asn Lys Glu Ala Leu Gln Ala Glu Val Gly Leu Pro Val Asp Arg
 305 310 315 320

Asn Ile Pro Leu Val Ala Phe Ile Gly Arg Leu Glu Glu Gln Lys Gly
 325 330 335

Pro Asp Val Met Ala Ala Ala Ile Pro Gln Leu Met Glu Met Val Glu
 340 345 350

Asp Val Gln Ile Val Leu Leu Gly Thr Gly Lys Lys Lys Phe Glu Arg
 355 360 365

Met Leu Met Ser Ala Glu Glu Lys Phe Pro Gly Lys Val Arg Ala Val
 370 375 380

Val Lys Phe Asn Ala Ala Leu Ala His His Ile Met Ala Gly Ala Asp
 385 390 395 400

Val Leu Ala Val Thr Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln Leu
 405 410 415

Gln Gly Met Arg Tyr Gly Thr Pro Cys Ala Cys Ala Ser Thr Gly Gly
 420 425 430

Leu Val Asp Thr Ile Ile Glu Gly Lys Thr Gly Phe His Met Gly Arg
 435 440 445

Leu Ser Val Asp Cys Asn Val Val Glu Pro Ala Asp Val Lys Lys Val
 450 455 460

Ala Thr Thr Leu Gln Arg Ala Ile Lys Val Val Gly Thr Pro Ala Tyr
 465 470 475 480

Glu Glu Met Val Arg Asn Cys Met Ile Gln Asp Leu Ser Trp Lys Gly
485 490 495

Pro Ala Lys Asn Trp Glu Asn Val Leu Leu Ser Leu Gly Val Ala Gly
500 505 510

Gly Glu Pro Gly Val Glu Gly Glu Ile Ala Pro Leu Ala Lys Glu
515 520 525

Asn Val Ala Ala Pro *
530

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Oryza sativa

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 453..2282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAATTCACTG TGAAGGAATA GATTCTCTTC AAAACAATTT AATCATTCCAT CTGATCTGCT	60
CAAAGCTCTG TGCATCTCCG GGTGCAACGG CCAGGATATT TATTGTGCAG TAAAAAAATG	120
TCATATCCCC TAGCCACCCA AGAAACTGCT CCTTAAGTCC TTATAAGCAC ATATGGCATT	180
GTAATATATA TGTTTGAGTT TTAGCGACAA TTTTTTTAAA AACTTTGGT CCTTTTTATG	240
AACGTTTAA GTTCACTGT CTTTTTTTT CGAATTTAA ATGTAGCTTC AAATTCTAAT	300
CCCCAATCCA AATTGTAATA AACTTCAATT CTCCTAATTA ACATCTTAAT TCATTTATTT	360

GAAACCAGT TCAAATTCTT TTTAGGCTCA CCAAACCTTA AACAAATTCAA TTCAGTGCAG	420		
AGATCTTCCA CAGCAACAGC TAGACAACCA CC ATG TCG GCT CTC ACC ACG TCC Met Ser Ala Leu Thr Thr Ser	473		
535	540		
CAG CTC GCC ACC TCG GCC ACC GGC TTC GGC ATC GCC GAC AGG TCG GCG Gln Leu Ala Thr Ser Ala Thr Gly Phe Gly Ile Ala Asp Arg Ser Ala	521		
545	550	555	
CCG TCG TCG CTG CTC CGC CAC GGG TTC CAG GGC CTC AAG CCC CGC AGC Pro Ser Ser Leu Leu Arg His Gly Phe Gln Gly Leu Lys Pro Arg Ser	569		
560	565	570	
CCC GCC GGC GGC GAC GCG ACG TCG CTC AGC GTG ACG ACC AGC GCG CGC Pro Ala Gly Gly Asp Ala Thr Ser Leu Ser Val Thr Thr Ser Ala Arg	617		
575	580	585	
GCG ACG CCC AAG CAG CAG CGG TCG GTG CAG CGT GGC AGC CGG AGG TTC Ala Thr Pro Lys Gln Gln Arg Ser Val Gln Arg Gly Ser Arg Arg Phe	665		
590	595	600	605
CCC TCC GTC GTC GTG TAC GCC ACC GGC GCC GGC ATG AAC GTC GTG TTC Pro Ser Val Val Val Tyr Ala Thr Gly Ala Gly Met Asn Val Val Phe	713		
610	615	620	
GTC GGC GCC GAG ATG GCC CCC TGG AGC AAG ACC GGC GGC CTC GGT GAC Val Gly Ala Glu Met Ala Pro Trp Ser Lys Thr Gly Gly Leu Gly Asp	761		
625	630	635	
GTC CTC GGT GGC CTC CCC CCT GCC ATG GCT GCG AAT GGC CAC AGG GTC Val Leu Gly Gly Leu Pro Pro Ala Met Ala Ala Asn Gly His Arg Val	809		
640	645	650	
ATG GTG ATC TCT CCT CGG TAC GAC CAG TAC AAG GAC GCT TGG GAT ACC Met Val Ile Ser Pro Arg Tyr Asp Gln Tyr Lys Asp Ala Trp Asp Thr	857		
655	660	665	
AGC GTT GTG GCT GAG ATC AAG GTT GCA GAC AGG TAC GAG AGG GTG AGG Ser Val Val Ala Glu Ile Lys Val Ala Asp Arg Tyr Glu Arg Val Arg	905		
670	675	680	685
TTT TTC CAT TGC TAC AAG CGT GGA GTC GAC CGT GTG TTC ATC GAC CAT Phe Phe His Cys Tyr Lys Arg Gly Val Asp Arg Val Phe Ile Asp His	953		
690	695	700	

CCG TCA TTC CTG GAG AAG GTT TGG GGA AAG ACC GGT GAG AAG ATC TAC Pro Ser Phe Leu Glu Lys Val Trp Gly Lys Thr Gly Glu Lys Ile Tyr 705 710 715	1001
GGA CCT GAC ACT GGA GTT GAT TAC AAA GAC AAC CAG ATG CGT TTC AGC Gly Pro Asp Thr Gly Val Asp Tyr Lys Asp Asn Gln Met Arg Phe Ser 720 725 730	1049
CTT CTT TGC CAG GCA GCA CTC GAG GCT CCT AGG ATC CTA AAC CTC AAC Leu Leu Cys Gln Ala Ala Leu Glu Ala Pro Arg Ile Leu Asn Leu Asn 735 740 745	1097
AAC AAC CCA TAC TTC AAA GGA ACT TAT GGT GAG GAT GTT GTG TTC GTC Asn Asn Pro Tyr Phe Lys Gly Thr Tyr Gly Glu Asp Val Val Phe Val 750 755 760 765	1145
TGC AAC GAC TGG CAC ACT GGC CCA CTG GCG AGC TAC CTG AAG AAC AAC Cys Asn Asp Trp His Thr Gly Pro Leu Ala Ser Tyr Leu Lys Asn Asn 770 775 780	1193
TAC CAG CCC AAT GGC ATC TAC AGG AAT GCA AAG GTT GCT TTC TGC ATC Tyr Gln Pro Asn Gly Ile Tyr Arg Asn Ala Lys Val Ala Phe Cys Ile 785 790 795	1241
CAC AAC ATC TCC TAC CAG GGC CGT TTC GCT TTC GAG GAT TAC CCT GAG His Asn Ile Ser Tyr Gln Gly Arg Phe Ala Phe Glu Asp Tyr Pro Glu 800 805 810	1289
CTG AAC CTC TCC GAG AGG TTC AGG TCA TCC TTC GAT TTC ATC GAC GGG Leu Asn Leu Ser Glu Arg Phe Arg Ser Ser Phe Asp Phe Ile Asp Gly 815 820 825	1337
TAT GAC ACG CCG GTG GAG GGC AGG AAG ATC AAC TGG ATG AAG GCC GGA Tyr Asp Thr Pro Val Glu Gly Arg Lys Ile Asn Trp Met Lys Ala Gly 830 835 840 845	1385
ATC CTG GAA GCC GAC AGG GTG CTC ACC GTG AGC CCG TAC TAC GCC GAG Ile Leu Glu Ala Asp Arg Val Leu Thr Val Ser Pro Tyr Tyr Ala Glu 850 855 860	1433
GAG CTC ATC TCC GGC ATC GCC AGG GGA TGC GAG CTC GAC AAC ATC ATG Glu Leu Ile Ser Gly Ile Ala Arg Gly Cys Glu Leu Asp Asn Ile Met 865 870 875	1481
CGG CTC ACC GGC ATC ACC GGC ATC GTC AAC GGC ATG GAC GTC AGC GAG	1529

Arg Leu Thr Gly Ile Thr Gly Ile Val Asn Gly Met Asp Val Ser Glu			
880	885	890	
TGG GAT CCT AGC AAG GAC AAG TAC ATC ACC GCC AAG TAC GAC GCA ACC			1577
Trp Asp Pro Ser Lys Asp Lys Tyr Ile Thr Ala Lys Tyr Asp Ala Thr			
895	900	905	
ACG GCA ATC GAG GCG AAG GCG CTG AAC AAG GAG GCG TTG CAG GCG GAG			1625
Thr Ala Ile Glu Ala Lys Ala Leu Asn Lys Glu Ala Leu Gln Ala Glu			
910	915	920	925
GCG GGT CTT CCG GTC GAC AGG AAA ATC CCA CTG ATC GCG TTC ATC GGC			1673
Ala Gly Leu Pro Val Asp Arg Lys Ile Pro Leu Ile Ala Phe Ile Gly			
930	935	940	
AGG CTG GAG GAA CAG AAG GGC CCT GAC GTC ATG GCC GCC GCC ATC CCG			1721
Arg Leu Glu Glu Gln Lys Gly Pro Asp Val Met Ala Ala Ile Pro			
945	950	955	
GAG CTC ATG CAG GAG GAC GTC CAG ATC GTT CTT CTG GGT ACT GGA AAG			1769
Glu Leu Met Gln Glu Asp Val Gln Ile Val Leu Leu Gly Thr Gly Lys			
960	965	970	
AAG AAG TTC GAG AAG CTG CTC AAG AGC ATG GAG GAG AAG TAT CCG GGC			1817
Lys Lys Phe Glu Lys Leu Leu Lys Ser Met Glu Glu Lys Tyr Pro Gly			
975	980	985	
AAG GTG AGG GCG GTG GTG AAG TTC AAC GCG CCG CTT GCT CAT CTC ATC			1865
Lys Val Arg Ala Val Val Lys Phe Asn Ala Pro Leu Ala His Leu Ile			
990	995	1000	1005
ATG GCC GGA GCC GAC GTG CTC GCC GTC CCC AGC CGC TTC GAG CCC TGT			1913
Met Ala Gly Ala Asp Val Leu Ala Val Pro Ser Arg Phe Glu Pro Cys			
1010	1015	1020	
GGA CTC ATC CAG CTG CAG GGG ATG AGA TAC GGA ACG CCC TGT GCT TGC			1961
Gly Leu Ile Gln Leu Gln Gly Met Arg Tyr Gly Thr Pro Cys Ala Cys			
1025	1030	1035	
GCG TCC ACC GGT GGG CTC GTG GAC ACG GTC ATC GAA GGC AAG ACT GGT			2009
Ala Ser Thr Gly Gly Leu Val Asp Thr Val Ile Glu Gly Lys Thr Gly			
1040	1045	1050	
TTC CAC ATG GGC CGT CTC AGC GTC GAC TGC AAG GTG GTG GAG CCA AGC			2057
Phe His Met Gly Arg Leu Ser Val Asp Cys Lys Val Val Glu Pro Ser			

1055	1060	1065	
GAC GTG AAG AAG GTG GCG GCC ACC CTG AAG CGC GCC ATC AAG GTC GTC			
Asp Val Lys Lys Val Ala Ala Thr Leu Lys Arg Ala Ile Lys Val Val			
1070	1075	1080	2105
1085			
GGC ACG CCG GCG TAC GAG GAG ATG GTC AGG AAC TGC ATG AAC CAG GAC			
Gly Thr Pro Ala Tyr Glu Glu Met Val Arg Asn Cys Met Asn Gln Asp			
1090	1095	1100	2153
CTC TCC TGG AAG GGG CCT GCG AAG AAC TGG GAG AAT GTG CTC CTG GGC			
Leu Ser Trp Lys Gly Pro Ala Lys Asn Trp Glu Asn Val Leu Leu Gly			
1105	1110	1115	2201
CTG GGC GTC GCC GGC AGC GCG CCG GGG ATC GAA GGC GAC GAG ATC GCG			
Leu Gly Val Ala Gly Ser Ala Pro Gly Ile Glu Gly Asp Glu Ile Ala			
1120	1125	1130	2249
CCG CTC GCC AAG GAG AAC GTG GCT GCT CCT TGA AGAGCCTGAG ATCTACATAT			
Pro Leu Ala Lys Glu Asn Val Ala Ala Pro *			
1135	1140		2302
GGAGTGATTA ATTAATATAG CAGTATATGG ATGAGAGACG AATGAACCAG TGGTTTGT			
TTGTAGTGA ATTTGTAGCT ATAGCCAATT ATATAGGCTA ATAAGTTGA TGTTGTACTC			
TTCTGGGTGT GCTTAAGTAT CTTATCGGAC CCTGAATTAA TGTGTGTGGC TTATTGCCAA			
TAATATTAAG TAATAAAGGG TTTATTATAT TATTATATAT GTTATATTAT ACTAAAAAAA			
2542			

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Ser	Ala	Leu	Thr	Thr	Ser	Gln	Leu	Ala	Thr	Ser	Ala	Thr	Gly	Phe
1		5						10					15		

Gly	Ile	Ala	Asp	Arg	Ser	Ala	Pro	Ser	Ser	Leu	Leu	Arg	His	Gly	Phe
	20				25							30			
Gln Gly Leu Lys Pro Arg Ser Pro Ala Gly Gly Asp Ala Thr Ser Leu															
	35			40			45								
Ser Val Thr Thr Ser Ala Arg Ala Thr Pro Lys Gln Gln Arg Ser Val,															
	50			55			60								
Gln Arg Gly Ser Arg Arg Phe Pro Ser Val Val Val Tyr Ala Thr Gly															
	65		70		75		80								
Ala Gly Met Asn Val Val Phe Val Gly Ala Glu Met Ala Pro Trp Ser															
	85			90			95								
Lys Thr Gly Gly Leu Gly Asp Val Leu Gly Gly Leu Pro Pro Ala Met															
	100			105			110								
Ala Ala Asn Gly His Arg Val Met Val Ile Ser Pro Arg Tyr Asp Gln															
	115			120			125								
Tyr Lys Asp Ala Trp Asp Thr Ser Val Val Ala Glu Ile Lys Val Ala															
	130		135		140										
Asp Arg Tyr Glu Arg Val Arg Phe Phe His Cys Tyr Lys Arg Gly Val															
	145		150		155		160								
Asp Arg Val Phe Ile Asp His Pro Ser Phe Leu Glu Lys Val Trp Gly															
	165			170			175								
Lys Thr Gly Glu Lys Ile Tyr Gly Pro Asp Thr Gly Val Asp Tyr Lys															
	180			185			190								
Asp Asn Gln Met Arg Phe Ser Leu Leu Cys Gln Ala Ala Leu Glu Ala															
	195			200			205								
Pro Arg Ile Leu Asn Leu Asn Asn Asn Pro Tyr Phe Lys Gly Thr Tyr															
	210		215		220										
Gly Glu Asp Val Val Phe Val Cys Asn Asp Trp His Thr Gly Pro Leu															
	225		230		235		240								
Ala Ser Tyr Leu Lys Asn Asn Tyr Gln Pro Asn Gly Ile Tyr Arg Asn															
	245			250			255								

Ala Lys Val Ala Phe Cys Ile His Asn Ile Ser Tyr Gln Gly Arg Phe
260 265 270

Ala Phe Glu Asp Tyr Pro Glu Leu Asn Leu Ser Glu Arg Phe Arg Ser
275 280 285

Ser Phe Asp Phe Ile Asp Gly Tyr Asp Thr Pro Val Glu Gly Arg Lys
290 295 300

Ile Asn Trp Met Lys Ala Gly Ile Leu Glu Ala Asp Arg Val Leu Thr
305 310 315 320

Val Ser Pro Tyr Tyr Ala Glu Glu Leu Ile Ser Gly Ile Ala Arg Gly
325 330 335

Cys Glu Leu Asp Asn Ile Met Arg Leu Thr Gly Ile Thr Gly Ile Val
340 345 350

Asn Gly Met Asp Val Ser Glu Trp Asp Pro Ser Lys Asp Lys Tyr Ile
355 360 365

Thr Ala Lys Tyr Asp Ala Thr Thr Ala Ile Glu Ala Lys Ala Leu Asn
370 375 380

Lys Glu Ala Leu Gln Ala Glu Ala Gly Leu Pro Val Asp Arg Lys Ile
385 390 395 400

Pro Leu Ile Ala Phe Ile Gly Arg Leu Glu Glu Gln Lys Gly Pro Asp
405 410 415

Val Met Ala Ala Ala Ile Pro Glu Leu Met Gln Glu Asp Val Gln Ile
420 425 430

Val Leu Leu Gly Thr Gly Lys Lys Phe Glu Lys Leu Leu Lys Ser
435 440 445

Met Glu Glu Lys Tyr Pro Gly Lys Val Arg Ala Val Val Lys Phe Asn
450 455 460

Ala Pro Leu Ala His Leu Ile Met Ala Gly Ala Asp Val Leu Ala Val
465 470 475 480

Pro Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln Leu Gln Gly Met Arg
485 490 495

Tyr Gly Thr Pro Cys Ala Cys Ala Ser Thr Gly Gly Leu Val Asp Thr
500 505 510

Val Ile Glu Gly Lys Thr Gly Phe His Met Gly Arg Leu Ser Val Asp
515 520 525

Cys Lys Val Val Glu Pro Ser Asp Val Lys Lys Val Ala Ala Thr Leu
530 535 540

Lys Arg Ala Ile Lys Val Val Gly Thr Pro Ala Tyr Glu Glu Met Val
545 550 555 560

Arg Asn Cys Met Asn Gln Asp Leu Ser Trp Lys Gly Pro Ala Lys Asn
565 570 575

Trp Glu Asn Val Leu Leu Gly Leu Gly Val Ala Gly Ser Ala Pro Gly
580 585 590

Ile Glu Gly Asp Glu Ile Ala Pro Leu Ala Lys Glu Asn Val Ala Ala
595 600 605

Pro *

610

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2007 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Zea mays

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCT GAG GCT GAG GCC GGG GGC AAG GAC GCG CCG CCG GAG AGG AGC GGC Ala Glu Ala Glu Ala Gly Gly Lys Asp Ala Pro Pro Glu Arg Ser Gly	615	620	625	48
GAC GCC GCC AGG TTG CCC CGC GCT CGG CGC AAT GCG GTC TCC AAA CGG Asp Ala Ala Arg Leu Pro Arg Ala Arg Arg Asn Ala Val Ser Lys Arg	630	635	640	96
AGG GAT CCT CTT CAG CCG GTC GGC CGG TAC GGC TCC GCG ACG GGA AAC Arg Asp Pro Leu Gln Pro Val Gly Arg Tyr Gly Ser Ala Thr Gly Asn	645	650	655	144
ACG GCC AGG ACC GGC GCC GCG TCC TGC CAG AAC GCC GCA TTG GCG GAC Thr Ala Arg Thr Gly Ala Ala Ser Cys Gln Asn Ala Ala Leu Ala Asp	660	665	670	192
GTT GAG ATC GTT GAG ATC AAG TCC ATC GTC GCC GCG CCG CCG ACG AGC Val Glu Ile Val Glu Ile Lys Ser Ile Val Ala Ala Pro Pro Thr Ser	675	680	685	240
ATA GTG AAG TTC CCA GGG CGC GGG CTA CAG GAT GAT CCT TCC CTC TGG Ile Val Lys Phe Pro Gly Arg Gly Leu Gln Asp Asp Pro Ser Leu Trp	695	700	705	288
GAC ATA GCA CCG GAG ACT GTC CTC CCA GCC CCG AAG CCA CTG CAT GAA Asp Ile Ala Pro Glu Thr Val Leu Pro Ala Pro Lys Pro Leu His Glu	710	715	720	336
TCG CCT GCG GTT GAC GGA GAT TCA AAT GGA ATT GCA CCT CCT ACA GTT Ser Pro Ala Val Asp Gly Asp Ser Asn Gly Ile Ala Pro Pro Thr Val	725	730	735	384
GAG CCA TTA GTA CAG GAG GCC ACT TGG GAT TTC AAG AAA TAC ATC GGT Glu Pro Leu Val Gln Glu Ala Thr Trp Asp Phe Lys Lys Tyr Ile Gly	740	745	750	432
TTT GAC GAG CCT GAC GAA GCG AAG GAT GAT TCC AGG GTT GGT GCA GAT Phe Asp Glu Pro Asp Glu Ala Lys Asp Asp Ser Arg Val Gly Ala Asp	755	760	765	480
GAT GCT GGT TCT TTT GAA CAT TAT GGG ACA ATG ATT CTG GGC CTT TGT Asp Ala Gly Ser Phe Glu His Tyr Gly Thr Met Ile Leu Gly Leu Cys	775	780	785	528
GGG GAG AAT GTT ATG AAC GTG ATC GTG GTG GCT GCT GAA TGT TCT CCA				576

Gly Glu Asn Val Met Asn Val Ile Val Val Ala Ala Glu Cys Ser Pro			
790	795	800	
TGG TGC AAA ACA GCA GGT CTT GGA GAT GTT GTG GGA GCT TTA CCC AAG			624
Trp Cys Lys Thr Gly Gly Leu Gly Asp Val Val Gly Ala Leu Pro Lys			
805	810	815	
GCT TTA GCG AGA AGA GGA CAT CGT GTT ATG GTT GTG GTA CCA AGG TAT			672
Ala Leu Ala Arg Arg Gly His Arg Val Met Val Val Val Pro Arg Tyr			
820	825	830	
GGG GAC TAT GTG GAA GCC TTT GAT ATG GGA ATC CGG AAA TAC TAC AAA			720
Gly Asp Tyr Val Glu Ala Phe Asp Met Gly Ile Arg Lys Tyr Tyr Lys			
835	840	845	850
GCT GCA GGA CAG GAC CTA GAA GTG AAC TAT TTC CAT GCA TTT ATT GAT			768
Ala Ala Gly Gln Asp Leu Glu Val Asn Tyr Phe His Ala Phe Ile Asp			
855	860	865	
GGA GTC GAC TTT GTG TTC ATT GAT GCC TCT TTC CGG CAC CGT CAA GAT			816
Gly Val Asp Phe Val Phe Ile Asp Ala Ser Phe Arg His Arg Gln Asp			
870	875	880	
GAC ATA TAT GGG GGA AGT AGG CAG GAA ATC ATG AAG CGC ATG ATT TTG			864
Asp Ile Tyr Gly Ser Arg Gln Glu Ile Met Lys Arg Met Ile Leu			
885	890	895	
TTT TGC AAG GTT GCT GTT GAG GTT CCT TGG CAC GTT CCA TGC GGT GGT			912
Phe Cys Lys Val Ala Val Glu Val Pro Trp His Val Pro Cys Gly Gly			
900	905	910	
GTG TGC TAC GGA GAT GGA AAT TTG GTG TTC ATT GCC ATG AAT TGG CAC			960
Val Cys Tyr Gly Asp Gly Asn Leu Val Phe Ile Ala Met Asn Trp His			
915	920	925	930
ACT GCA CTC CTG CCT GTT TAT CTG AAG GCA TAT TAC AGA GAC CAT GGG			1008
Thr Ala Leu Leu Pro Val Tyr Leu Lys Ala Tyr Tyr Arg Asp His Gly			
935	940	945	
TTA ATG CAG TAC ACT CGC TCC GTC CTC GTC ATA CAT AAC ATC GGC CAC			1056
Leu Met Gln Tyr Thr Arg Ser Val Leu Val Ile His Asn Ile Gly His			
950	955	960	
CAG GGC CGT GGT CCT GTA CAT GAA TTC CCG TAC ATG GAC TTG CTG AAC			1104
Gln Gly Arg Gly Pro Val His Glu Phe Pro Tyr Met Asp Leu Leu Asn			

965	970	975	
ACT AAC CTT CAA CAT TTC GAG CTG TAC GAT CCC GTC GGT GGC GAG CAC Thr Asn Leu Gln His Phe Glu Leu Tyr Asp Pro Val Gly Gly Glu His			1152
980	985	990	
GCC AAC ATC TTT GCC GCG TGT GTT CTG AAG ATG GCA GAC CGG GTG GTG Ala Asn Ile Phe Ala Ala Cys Val Leu Lys Met Ala Asp Arg Val Val			1200
995	1000	1005	1010
ACT GTC AGC CGC GGC TAC CTG TGG GAG CTG AAG ACA GTG GAA GGC GGC Thr Val Ser Arg Gly Tyr Leu Trp Glu Leu Lys Thr Val Glu Gly Gly			1248
1015	1020	1025	
TGG GGC CTC CAC GAC ATC ATC CGT TCT AAC GAC TGG AAG ATC AAT GGC Trp Gly Leu His Asp Ile Ile Arg Ser Asn Asp Trp Lys Ile Asn Gly			1296
1030	1035	1040	
ATT CGT GAA CGC ATC GAC CAC CAG GAG TGG AAC CCC AAG GTG GAC GTG Ile Arg Glu Arg Ile Asp His Gln Glu Trp Asn Pro Lys Val Asp Val			1344
1045	1050	1055	
CAC CTG CGG TCG GAC GGC TAC ACC AAC TAC TCC CTC GAG ACA CTC GAC His Leu Arg Ser Asp Gly Tyr Thr Asn Tyr Ser Leu Glu Thr Leu Asp			1392
1060	1065	1070	
GCT GGA AAG CGG CAG TGC AAG GCG GCC CTG CAG CGG GAC GTG GGC CTG Ala Gly Lys Arg Gln Cys Lys Ala Ala Leu Gln Arg Asp Val Gly Leu			1440
1075	1080	1085	1090
GAA GTG CGC GAC GAC GTG CCG CTG CTC GGC TTC ATC GGG CGT CTG GAT Glu Val Arg Asp Asp Val Pro Leu Leu Gly Phe Ile Gly Arg Leu Asp			1488
1095	1100	1105	
GGA CAG AAG GGC GTG GAC ATC ATC GGG GAC GCG ATG CCG TGG ATC GCG Gly Gln Lys Gly Val Asp Ile Ile Gly Asp Ala Met Pro Trp Ile Ala			1536
1110	1115	1120	
GGG CAG GAC GTG CAG CTG GTG ATG CTG GGC ACC GGC CCA CCT GAC CTG Gly Gln Asp Val Gln Leu Val Met Leu Gly Thr Gly Pro Pro Asp Leu			1584
1125	1130	1135	
GAA CGA ATG CTG CAG CAC TTG GAG CGG GAG CAT CCC AAC AAG GTG CGC Glu Arg Met Leu Gln His Leu Glu Arg Glu His Pro Asn Lys Val Arg			1632
1140	1145	1150	

GGG TGG GTC GGG TTC TCG GTC CTA ATG GTG CAT CGC ATC ACG CCG GGC Gly Trp Val Gly Phe Ser Val Leu Met Val His Arg Ile Thr Pro Gly	1155	1160	1165	1170	1680
GCC AGC GTG CTG GTG ATG CCC TCC CGC TTC GCC GGC GGG CTG AAC CAG Ala Ser Val Leu Val Met Pro Ser Arg Phe Ala Gly Gly Leu Asn Gln	1175	1180		1185	1728
CTC TAC GCG ATG GCA TAC GGC ACC GTC CCT GTG GTG CAC GCC GTG GGC Leu Tyr Ala Met Ala Tyr Gly Thr Val Pro Val Val His Ala Val Gly	1190	1195		1200	1776
GGG CTC AGG GAC ACC GTG GCG CCG TTC GAC CCG TTC GGC GAC GCC GGG Gly Leu Arg Asp Thr Val Ala Pro Phe Asp Pro Phe Gly Asp Ala Gly	1205	1210		1215	1824
CTC GGG TGG ACT TTT GAC CGC GCC GAG GCC AAC AAG CTG ATC GAG GTG Leu Gly Trp Thr Phe Asp Arg Ala Glu Ala Asn Lys Leu Ile Glu Val	1220	1225		1230	1872
CTC AGC CAC TGC CTC GAC ACG TAC CGA AAC TAC GAG GAG AGC TGG AAG Leu Ser His Cys Leu Asp Thr Tyr Arg Asn Tyr Glu Glu Ser Trp Lys	1235	1240	1245	1250	1920
AGT CTC CAG GCG CGC GGC ATG TCG CAG AAC CTC AGC TGG GAC CAC GCG Ser Leu Gln Ala Arg Gly Met Ser Gln Asn Leu Ser Trp Asp His Ala	1255	1260		1265	1968
GCT GAG CTC TAC GAG GAC GTC CTT GTC AAG TAC CAG TGG Ala Glu Leu Tyr Glu Asp Val Leu Val Lys Tyr Gln Trp	1270	1275			2007

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ala Glu Ala Glu Ala Gly Gly Lys Asp Ala Pro Pro Glu Arg Ser Gly

1

5

10

15

Asp Ala Ala Arg Leu Pro Arg Ala Arg Arg Asn Ala Val Ser Lys Arg
20 25 30

Arg Asp Pro Leu Gln Pro Val Gly Arg Tyr Gly Ser Ala Thr Gly Asn
35 40 45

Thr Ala Arg Thr Gly Ala Ala Ser Cys Gln Asn Ala Ala Leu Ala Asp
50 55 60

Val Glu Ile Val Glu Ile Lys Ser Ile Val Ala Ala Pro Pro Thr Ser
65 70 75 80

Ile Val Lys Phe Pro Gly Arg Gly Leu Gln Asp Asp Pro Ser Leu Trp
85 90 95

Asp Ile Ala Pro Glu Thr Val Leu Pro Ala Pro Lys Pro Leu His Glu
100 105 110

Ser Pro Ala Val Asp Gly Asp Ser Asn Gly Ile Ala Pro Pro Thr Val
115 120 125

Glu Pro Leu Val Gln Glu Ala Thr Trp Asp Phe Lys Lys Tyr Ile Gly
130 135 140

Phe Asp Glu Pro Asp Glu Ala Lys Asp Asp Ser Arg Val Gly Ala Asp
145 150 155 160

Asp Ala Gly Ser Phe Glu His Tyr Gly Thr Met Ile Leu Gly Leu Cys
165 170 175

Gly Glu Asn Val Met Asn Val Ile Val Val Ala Ala Glu Cys Ser Pro
180 185 190

Trp Cys Lys Thr Gly Gly Leu Gly Asp Val Val Gly Ala Leu Pro Lys
195 200 205

Ala Leu Ala Arg Arg Gly His Arg Val Met Val Val Val Pro Arg Tyr
210 215 220

Gly Asp Tyr Val Glu Ala Phe Asp Met Gly Ile Arg Lys Tyr Tyr Lys
225 230 235 240

Ala Ala Gly Gln Asp Leu Glu Val Asn Tyr Phe His Ala Phe Ile Asp

	245	250	255
Gly Val Asp Phe Val Phe Ile Asp Ala Ser Phe Arg His Arg Gln Asp			
260	265	270	
Asp Ile Tyr Gly Gly Ser Arg Gln Glu Ile Met Lys Arg Met Ile Leu			
275	280	285	
Phe Cys Lys Val Ala Val Glu Val Pro Trp His Val Pro Cys Gly Gly			
290	295	300	
Val Cys Tyr Gly Asp Gly Asn Leu Val Phe Ile Ala Met Asn Trp His			
305	310	315	320
Thr Ala Leu Leu Pro Val Tyr Leu Lys Ala Tyr Tyr Arg Asp His Gly			
325	330	335	
Leu Met Gln Tyr Thr Arg Ser Val Leu Val Ile His Asn Ile Gly His			
340	345	350	
Gln Gly Arg Gly Pro Val His Glu Phe Pro Tyr Met Asp Leu Leu Asn			
355	360	365	
Thr Asn Leu Gln His Phe Glu Leu Tyr Asp Pro Val Gly Gly Glu His			
370	375	380	
Ala Asn Ile Phe Ala Ala Cys Val Leu Lys Met Ala Asp Arg Val Val			
385	390	395	400
Thr Val Ser Arg Gly Tyr Leu Trp Glu Leu Lys Thr Val Glu Gly Gly			
405	410	415	
Trp Gly Leu His Asp Ile Ile Arg Ser Asn Asp Trp Lys Ile Asn Gly			
420	425	430	
Ile Arg Glu Arg Ile Asp His Gln Glu Trp Asn Pro Lys Val Asp Val			
435	440	445	
His Leu Arg Ser Asp Gly Tyr Thr Asn Tyr Ser Leu Glu Thr Leu Asp			
450	455	460	
Ala Gly Lys Arg Gln Cys Lys Ala Ala Leu Gln Arg Asp Val Gly Leu			
465	470	475	480
Glu Val Arg Asp Asp Val Pro Leu Leu Gly Phe Ile Gly Arg Leu Asp			

485	490	495
Gly Gln Lys Gly Val Asp Ile Ile Gly Asp Ala Met Pro Trp Ile Ala		
500	505	510
Gly Gln Asp Val Gln Leu Val Met Leu Gly Thr Gly Pro Pro Asp Leu		
515	520	525
Glu Arg Met Leu Gln His Leu Glu Arg Glu His Pro Asn Lys Val Arg		
530	535	540
Gly Trp Val Gly Phe Ser Val Leu Met Val His Arg Ile Thr Pro Gly		
545	550	555
Ala Ser Val Leu Val Met Pro Ser Arg Phe Ala Gly Gly Leu Asn Gln		
565	570	575
Leu Tyr Ala Met Ala Tyr Gly Thr Val Pro Val Val His Ala Val Gly		
580	585	590
Gly Leu Arg Asp Thr Val Ala Pro Phe Asp Pro Phe Gly Asp Ala Gly		
595	600	605
Leu Gly Trp Thr Phe Asp Arg Ala Glu Ala Asn Lys Leu Ile Glu Val		
610	615	620
Leu Ser His Cys Leu Asp Thr Tyr Arg Asn Tyr Glu Glu Ser Trp Lys		
625	630	635
Ser Leu Gln Ala Arg Gly Met Ser Gln Asn Leu Ser Trp Asp His Ala		
645	650	655
Ala Glu Leu Tyr Glu Asp Val Leu Val Lys Tyr Gln Trp		
660	665	

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2097 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Zea mays

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..2097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG CCG GGG GCA ATC TCT TCC TCG TCG GCT TTT CTC CTC CCC GTC Met Pro Gly Ala Ile Ser Ser Ser Ser Ala Phe Leu Leu Pro Val	48
670 675 680 685	
 GCG TCC TCC TCG CCG CGG CGC AGG CGG GGC AGT GTG GGT GCT GCT CTG Ala Ser Ser Pro Arg Arg Arg Arg Gly Ser Val Gly Ala Ala Leu	96
690 695 700	
 CGC TCG TAC GGC TAC AGC GGC GCG GAG CTG CGG TTG CAT TGG GCG CGG Arg Ser Tyr Gly Tyr Ser Gly Ala Glu Leu Arg Leu His Trp Ala Arg	144
705 710 715	
 CGG GGC CCG CCT CAG GAT GGA GCG GCG TCG GTA CGC GCC GCA GCG GCA Arg Gly Pro Pro Gln Asp Gly Ala Ala Ser Val Arg Ala Ala Ala	192
720 725 730	
 CCG GCC GGG GGC GAA AGC GAG GAG GCA GCG AAG AGC TCC TCC TCG TCC Pro Ala Gly Gly Glu Ser Glu Ala Ala Lys Ser Ser Ser Ser Ser	240
735 740 745	
 CAG GCG GGC GCT GTT CAG GGC AGC ACG GCC AAG GCT GTG GAT TCT GCT Gln Ala Gly Ala Val Gln Gly Ser Thr Ala Lys Ala Val Asp Ser Ala	288
750 755 760 765	
 TCA CCT CCC AAT CCT TTG ACA TCT GCT CCG AAG CAA AGT CAG AGC GCT Ser Pro Pro Asn Pro Leu Thr Ser Ala Pro Lys Gln Ser Gln Ser Ala	336
770 775 780	
 GCA ATG CAA AAC GGA ACG AGT GGG GGC AGC AGC GCG AGC ACC GCC GCG Ala Met Gln Asn Gly Thr Ser Gly Gly Ser Ser Ala Ser Thr Ala Ala	384
785 790 795	
 CCG GTG TCC GGA CCC AAA GCT GAT CAT CCA TCA GCT CCT GTC ACC AAG	432

Pro Val Ser Gly Pro Lys Ala Asp His Pro Ser Ala Pro Val Thr Lys			
800	805	810	
AGA GAA ATC GAT GCC AGT GCG GTG AAG CCA GAG CCC GCA GGT GAT GAT			480
Arg Glu Ile Asp Ala Ser Ala Val Lys Pro Glu Pro Ala Gly Asp Asp			
815	820	825	
GCT AGA CCG GTG GAA AGC ATA GGC ATC GCT GAA CCG GTG GAT GCT AAG			528
Ala Arg Pro Val Glu Ser Ile Gly Ile Ala Glu Pro Val Asp Ala Lys			
830	835	840	845
GCT GAT GCA GCT CCG GCT ACA GAT GCG GCG AGT GCT CCT TAT GAC			576
Ala Asp Ala Ala Pro Ala Thr Asp Ala Ala Ser Ala Pro Tyr Asp			
850	855	860	
AGG GAG GAT AAT GAA CCT GGC CCT TTG GCT GGG CCT AAT GTG ATG AAC			624
Arg Glu Asp Asn Glu Pro Gly Pro Leu Ala Gly Pro Asn Val Met Asn			
865	870	875	
GTC GTC GTG GTG GCT TCT GAA TGT GCT CCT TTC TGC AAG ACA GGT GGC			672
Val Val Val Ala Ser Glu Cys Ala Pro Phe Cys Lys Thr Gly Gly			
880	885	890	
CTT GGA GAT GTC GTG GGT GCT TTG CCT AAG GCT CTG GCG AGG AGA GGA			720
Leu Gly Asp Val Val Gly Ala Leu Pro Lys Ala Leu Ala Arg Arg Gly			
895	900	905	
CAC CGT GTT ATG GTC GTG ATA CCA AGA TAT GGA GAG TAT GCC GAA GCC			768
His Arg Val Met Val Val Ile Pro Arg Tyr Gly Glu Tyr Ala Glu Ala			
910	915	920	925
CGG GAT TTA GGT GTA AGG AGA CGT TAC AAG GTA GCT GGA CAG GAT TCA			816
Arg Asp Leu Gly Val Arg Arg Tyr Lys Val Ala Gly Gln Asp Ser			
930	935	940	
GAA GTT ACT TAT TTT CAC TCT TAC ATT GAT GGA GTT GAT TTT GTA TTC			864
Glu Val Thr Tyr Phe His Ser Tyr Ile Asp Gly Val Asp Phe Val Phe			
945	950	955	
GTA GAA GCC CCT CCC TTC CGG CAC CGG CAC AAT AAT ATT TAT GGG GGA			912
Val Glu Ala Pro Pro Phe Arg His Arg His Asn Asn Ile Tyr Gly Gly			
960	965	970	
GAA AGA TTG GAT ATT TTG AAG CGC ATG ATT TTG TTC TGC AAG GCC GCT			960
Glu Arg Leu Asp Ile Leu Lys Arg Met Ile Leu Phe Cys Lys Ala Ala			

975	980	985	
GTT GAG GTT CCA TGG TAT GCT CCA TGT GGC GGT ACT GTC TAT GGT GAT Val Glu Val Pro Trp Tyr Ala Pro Cys Gly Gly Thr Val Tyr Gly Asp			1008
990	995	1000	1005
GTC AAC TTA GTT TTC ATT GCT AAT GAT TGG CAT ACC GCA CTT CTG CCT Gly Asn Leu Val Phe Ile Ala Asn Asp Trp His Thr Ala Leu Leu Pro			1056
1010	1015	1020	
GTC TAT CTA AAG GCC TAT TAC CGG GAC AAT GGT TTG ATG CAG TAT GCT Val Tyr Leu Lys Ala Tyr Tyr Arg Asp Asn Gly Leu Met Gln Tyr Ala			1104
1025	1030	1035	
CGC TCT GTG CTT GTG ATA CAC AAC ATT GCT CAT CAG GGT CGT GGC CCT Arg Ser Val Leu Val Ile His Asn Ile Ala His Gln Gly Arg Gly Pro			1152
1040	1045	1050	
GTA GAC GAC TTC GTC AAT TTT GAC TTG CCT GAA CAC TAC ATC GAC CAC Val Asp Asp Phe Val Asn Phe Asp Leu Pro Glu His Tyr Ile Asp His			1200
1055	1060	1065	
TTC AAA CTG TAT GAC AAC ATT GGT GGG GAT CAC AGC AAC GTT TTT GCT Phe Lys Leu Tyr Asp Asn Ile Gly Gly Asp His Ser Asn Val Phe Ala			1248
1070	1075	1080	1085
GCG GGG CTG AAG ACG GCA GAC CGG GTG GTG ACC GTT AGC AAT GGC TAC Ala Gly Leu Lys Thr Ala Asp Arg Val Val Thr Val Ser Asn Gly Tyr			1296
1090	1095	1100	
ATG TGG GAG CTG AAG ACT TCG GAA GGC GGG TGG GGC CTC CAC GAC ATC Met Trp Glu Leu Lys Thr Ser Glu Gly Trp Gly Leu His Asp Ile			1344
1105	1110	1115	
ATA AAC CAG AAC GAC TGG AAG CTG CAG GGC ATC GTG AAC GGC ATC GAC Ile Asn Gln Asn Asp Trp Lys Leu Gln Gly Ile Val Asn Gly Ile Asp			1392
1120	1125	1130	
ATG AGC GAG TGG AAC CCC GCT GTG GAC GTG CAC CTC CAC TCC GAC GAC Met Ser Glu Trp Asn Pro Ala Val Asp Val His Leu His Ser Asp Asp			1440
1135	1140	1145	
TAC ACC AAC TAC ACG TTC GAG ACG CTG GAC ACC GGC AAG CGG CAG TGC Tyr Thr Asn Tyr Thr Phe Glu Thr Leu Asp Thr Gly Lys Arg Gln Cys			1488
1150	1155	1160	1165

AAG GCC GCC CTG CAG CGG CAG CTG GCG CTG CAG GTC CGC GAC GAC GTG		1536
Lys Ala Ala Leu Gln Arg Gln Leu Gly Le. Gln Val Arg Asp Asp Val		
1170	1175	1180
CCA CTG ATC GGG TTC ATC GGG CGG CTG GAC CAC CAG AAG GCG GTG GAC		1584
Pro Leu Ile Gly Phe Ile Gly Arg Leu Asp His Gln Lys Gly Val Asp		
1185	1190	1195
ATC ATC GCC GAC GCG ATC CAC TGG ATC GCG GGG CAG GAC GTG CAG CTC		1632
Ile Ile Ala Asp Ala Ile His Trp Ile Ala Gly Gln Asp Val Gln Leu		
1200	1205	1210
GTG ATG CTG GGC ACC GGG CGG GCC GAC CTG GAG GAC ATG CTG CGG CGG		1680
Val Met Leu Gly Thr Gly Arg Ala Asp Leu Glu Asp Met Leu Arg Arg		
1215	1220	1225
TTC GAG TCG GAG CAC AGC GAC AAG GTG CGC GCG TGG GTG GGG TTC TCG		1728
Phe Glu Ser Glu His Ser Asp Lys Val Arg Ala Trp Val Gly Phe Ser		
1230	1235	1240
1245		
GTG CCC CTG GCG CAC CGC ATC ACG GCG GGC GCG GAC ATC CTG CTG ATG		1776
Val Pro Leu Ala His Arg Ile Thr Ala Gly Ala Asp Ile Leu Leu Met		
1250	1255	1260
CCG TCG CGG TTC GAG CCG TGC GGG CTG AAC CAG CTC TAC GCC ATG GCG		1824
Pro Ser Arg Phe Glu Pro Cys Gly Leu Asn Gln Leu Tyr Ala Met Ala		
1265	1270	1275
TAC GGG ACC GTG CCC GTG GTG CAC GCC GTG GGG GGG CTC CGG GAC ACG		1872
Tyr Gly Thr Val Pro Val Val His Ala Val Gly Gly Leu Arg Asp Thr		
1280	1285	1290
GTG GCG CCG TTC GAC CCG TTC AAC GAC ACC GGG CTC GGG TGG ACG TTC		1920
Val Ala Pro Phe Asp Pro Phe Asn Asp Thr Gly Leu Gly Trp Thr Phe		
1295	1300	1305
GAC CGC GCG GAG GCG AAC CGG ATG ATC GAC GCG CTC TCG CAC TGC CTC		1968
Asp Arg Ala Glu Ala Asn Arg Met Ile Asp Ala Leu Ser His Cys Leu		
1310	1315	1320
1325		
ACC ACG TAC CGG AAC TAC AAG GAG AGC TGG CGC GCC TGC AGG GCG CGC		2016
Thr Thr Tyr Arg Asn Tyr Lys Glu Ser Trp Arg Ala Cys Arg Ala Arg		
1330	1335	1340
GGC ATG GCC GAG GAC CTC AGC TGG GAC CAC GCC GCC GTG CTG TAT GAG		2064

Gly Met Ala Glu Asp Leu Ser Trp Asp His Ala Ala Val Leu Tyr Glu
1345 1350 1355

GAC GTG CTC GTC AAG GCG AAG TAC CAG TGG TGA 2097
Asp Val Leu Val Lys Ala Lys Tyr Gln Trp *
1360 1365

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Pro Gly Ala Ile Ser Ser Ser Ser Ala Phe Leu Leu Pro Val
1 5 10 15

Ala Ser Ser Ser Pro Arg Arg Arg Arg Gly Ser Val Gly Ala Ala Leu
20 25 30

Arg Ser Tyr Gly Tyr Ser Gly Ala Glu Leu Arg Leu His Trp Ala Arg
35 40 45

Arg Gly Pro Pro Gln Asp Gly Ala Ala Ser Val Arg Ala Ala Ala
50 55 60

Pro Ala Gly Gly Glu Ser Glu Glu Ala Ala Lys Ser Ser Ser Ser
65 70 75 80

Gln Ala Gly Ala Val Gln Gly Ser Thr Ala Lys Ala Val Asp Ser Ala
85 90 95

Ser Pro Pro Asn Pro Leu Thr Ser Ala Pro Lys Gln Ser Gln Ser Ala
100 105 110

Ala Met Gln Asn Gly Thr Ser Gly Gly Ser Ser Ala Ser Thr Ala Ala
115 120 125

Pro Val Ser Gly Pro Lys Ala Asp His Pro Ser Ala Pro Val Thr Lys
130 135 140

Arg Glu Ile Asp Ala Ser Ala Val Lys Pro Glu Pro Ala Gly Asp Asp
145 150 155 160

Ala Arg Pro Val Glu Ser Ile Gly Ile Ala Glu Pro Val Asp Ala Lys
165 170 175

Ala Asp Ala Ala Pro Ala Thr Asp Ala Ala Ala Ser Ala Pro Tyr Asp
180 185 190

Arg Glu Asp Asn Glu Pro Gly Pro Leu Ala Gly Pro Asn Val Met Asn
195 200 205

Val Val Val Val Ala Ser Glu Cys Ala Pro Phe Cys Lys Thr Gly Gly
210 215 220

Leu Gly Asp Val Val Gly Ala Leu Pro Lys Ala Leu Ala Arg Arg Gly
225 230 235 240

His Arg Val Met Val Val Ile Pro Arg Tyr Gly Glu Tyr Ala Glu Ala
245 250 255

Arg Asp Leu Gly Val Arg Arg Arg Tyr Lys Val Ala Gly Gln Asp Ser
260 265 270

Glu Val Thr Tyr Phe His Ser Tyr Ile Asp Gly Val Asp Phe Val Phe
275 280 285

Val Glu Ala Pro Pro Phe Arg His Arg His Asn Asn Ile Tyr Gly Gly
290 295 300

Glu Arg Leu Asp Ile Leu Lys Arg Met Ile Leu Phe Cys Lys Ala Ala
305 310 315 320

Val Glu Val Pro Trp Tyr Ala Pro Cys Gly Gly Thr Val Tyr Gly Asp
325 330 335

Gly Asn Leu Val Phe Ile Ala Asn Asp Trp His Thr Ala Leu Leu Pro
340 345 350

Val Tyr Leu Lys Ala Tyr Tyr Arg Asp Asn Gly Leu Met Gln Tyr Ala
355 360 365

Arg Ser Val Leu Val Ile His Asn Ile Ala His Gln Gly Arg Gly Pro
370 375 380

Val Asp Asp Phe Val Asn Phe Asp Leu Pro Glu His Tyr Ile Asp His
385 390 395 400

Phe Lys Leu Tyr Asp Asn Ile Gly Gly Asp His Ser Asn Val Phe Ala
405 410 415

Ala Gly Leu Lys Thr Ala Asp Arg Val Val Thr Val Ser Asn Gly Tyr
420 425 430

Met Trp Glu Leu Lys Thr Ser Glu Gly Gly Trp Gly Leu His Asp Ile
435 440 445

Ile Asn Gln Asn Asp Trp Lys Leu Gln Gly Ile Val Asn Gly Ile Asp
450 455 460

Met Ser Glu Trp Asn Pro Ala Val Asp Val His Leu His Ser Asp Asp
465 470 475 480

Tyr Thr Asn Tyr Thr Phe Glu Thr Leu Asp Thr Gly Lys Arg Gln Cys
485 490 495

Lys Ala Ala Leu Gln Arg Gln Leu Gly Leu Gln Val Arg Asp Asp Val
500 505 510

Pro Leu Ile Gly Phe Ile Gly Arg Leu Asp His Gln Lys Gly Val Asp
515 520 525

Ile Ile Ala Asp Ala Ile His Trp Ile Ala Gly Gln Asp Val Gln Leu
530 535 540

Val Met Leu Gly Thr Gly Arg Ala Asp Leu Glu Asp Met Leu Arg Arg
545 550 555 560

Phe Glu Ser Glu His Ser Asp Lys Val Arg Ala Trp Val Gly Phe Ser
565 570 575

Val Pro Leu Ala His Arg Ile Thr Ala Gly Ala Asp Ile Leu Leu Met
580 585 590

Pro Ser Arg Phe Glu Pro Cys Gly Leu Asn Gln Leu Tyr Ala Met Ala
595 600 605

Tyr Gly Thr Val Pro Val Val His Ala Val Gly Gly Leu Arg Asp Thr
610 615 620

Val Ala Pro Phe Asp Pro Phe Asn Asp Thr Gly Leu Gly Trp Thr Phe
625 630 635 640

Asp Arg Ala Glu Ala Asn Arg Met Ile Asp Ala Leu Ser His Cys Leu
645 650 655

Thr Thr Tyr Arg Asn Tyr Lys Glu Ser Trp Arg Ala Cys Arg Ala Arg
660 665 670

Gly Met Ala Glu Asp Leu Ser Trp Asp His Ala Ala Val Leu Tyr Glu
675 680 685

Asp Val Leu Val Lys Ala Lys Tyr Gln Trp *

690 695

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Zea mays

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGC GTC GCG GAG CTG AGC AGG GAG GGG CCC GCG CCG CGC CCG CTG CCA 48
Cys Val Ala Glu Leu Ser Arg Glu Gly Pro Ala Pro Arg Pro Leu Pro
700 705 710 715

CCC GCG CTG CTG GCG CCC CCG CTC GTG CCC GGC TTC CTC GCG CCG CCG 96
Pro Ala Leu Leu Ala Pro Pro Leu Val Pro Gly Phe Leu Ala Pro Pro
720 725 730

GCC GAG CCC ACG GGT GAG CCG GCA TCG ACG CCG CCG CCC GTG CCC GAC Ala Glu Pro Thr Gly Glu Pro Ala Ser Thr Pro Pro Pro Val Pro Asp	735	740	745	144
GCC GGC CTG GGG GAC CTC GGT CTC GAA CCT GAA GGG ATT GCT GAA GGT Ala Gly Leu Gly Asp Leu Gly Leu Glu Pro Glu Gly Ile Ala Glu Gly	750	755	760	192
TCC ATC GAT AAC ACA GTA GTT GTG GCA AGT GAG CAA GAT TCT GAG ATT Ser Ile Asp Asn Thr Val Val Ala Ser Glu Gln Asp Ser Glu Ile	765	770	775	240
GTG GTT GGA AAG GAG CAA GCT CGA GCT AAA GTA ACA CAA AGC ATT GTC Val Val Gly Lys Glu Gln Ala Arg Ala Lys Val Thr Gln Ser Ile Val	780	785	790	795
TTT GTA ACC GGC GAA GCT TCT CCT TAT GCA AAG TCT GGG GGT CTA GGA Phe Val Thr Gly Glu Ala Ser Pro Tyr Ala Lys Ser Gly Gly Leu Gly	800	805	810	336
GAT GTT TGT GGT TCA TTG CCA GTT GCT CTT GCT GCT CGT GGT CAC CGT Asp Val Cys Gly Ser Leu Pro Val Ala Leu Ala Ala Arg Gly His Arg	815	820	825	384
GTG ATG GTT GTA ATG CCC AGA TAT TTA AAT GGT ACC TCC GAT AAG AAT Val Met Val Val Met Pro Arg Tyr Leu Asn Gly Thr Ser Asp Lys Asn	830	835	840	432
TAT GCA AAT GCA TTT TAC ACA GAA AAA CAC ATT CGG ATT CCA TGC TTT Tyr Ala Asn Ala Phe Tyr Thr Glu Lys His Ile Arg Ile Pro Cys Phe	845	850	855	480
GGC GGT GAA CAT GAA GTT ACC TTC TTC CAT GAG TAT AGA GAT TCA GTT Gly Gly Glu His Glu Val Thr Phe Phe His Glu Tyr Arg Asp Ser Val	860	865	870	528
GAC TGG GTG TTT GTT GAT CAT CCC TCA TAT CAC AGA CCT GGA AAT TTA Asp Trp Val Phe Val Asp His Pro Ser Tyr His Arg Pro Gly Asn Leu	880	885	890	576
TAT GGA GAT AAG TTT GGT GCT TTT GGT GAT AAT CAG TTC AGA TAC ACA Tyr Gly Asp Lys Phe Gly Ala Phe Gly Asp Asn Gln Phe Arg Tyr Thr	895	900	905	624
CTC CTT TGC TAT GCT GCA TGT GAG GCT CCT TTG ATC CTT GAA TTG GGA	672			

Leu	Leu	Cys	Tyr	Ala	Ala	Cys	Glu	Ala	Pro	Leu	Ile	Leu	Glu	Leu	Gly	
910																915
																920
GGA TAT ATT TAT GGA CAG AAT TGC ATG TTT GTT GTC AAT GAT TGG CAT															720	
Gly	Tyr	Ile	Tyr	Gly	Gln	Asn	Cys	Met	Phe	Val	Val	Asn	Asp	Trp	His	
925																930
																935
GCC AGT CTA GTG CCA GTC CTT GCT GCA AAA TAT AGA CCA TAT GGT															768	
Ala	Ser	Leu	Val	Pro	Val	Leu	Leu	Ala	Ala	Lys	Tyr	Arg	Pro	Tyr	Gly	
940																945
																950
																955
GTT TAT AAA GAC TCC CGC AGC ATT CTT GTA ATA CAT AAT TTA GCA CAT															816	
Val	Tyr	Lys	Asp	Ser	Arg	Ser	Ile	Leu	Val	Ile	His	Asn	Leu	Ala	His	
960																965
																970
CAG GGT GTA GAG CCT GCA AGC ACA TAT CCT GAC CTT GGG TTG CCA CCT															864	
Gln	Gly	Val	Glu	Pro	Ala	Ser	Thr	Tyr	Pro	Asp	Leu	Gly	Leu	Pro	Pro	
975																980
																985
GAA TGG TAT GGA GCT CTG GAG TGG GTA TTC CCT GAA TGG GCG AGG AGG															912	
Glu	Trp	Tyr	Gly	Ala	Leu	Glu	Trp	Val	Phe	Pro	Glu	Trp	Ala	Arg	Arg	
990																995
																1000
CAT GCC CTT GAC AAG GGT GAG GCA GTT AAT TTT TTG AAA GGT GCA GTT															960	
His	Ala	Leu	Asp	Lys	Gly	Glu	Ala	Val	Asn	Phe	Leu	Lys	Gly	Ala	Val	
1005																1010
																1015
GTG ACA GCA GAT CGA ATC GTG ACT GTC AGT AAG GGT TAT TCG TGG GAG															1008	
Val	Thr	Ala	Asp	Arg	Ile	Val	Thr	Val	Ser	Lys	Gly	Tyr	Ser	Trp	Glu	
1020																1025
																1030
																1035
GTC ACA ACT GCT GAA GGT GGA CAG GGC CTC AAT GAG CTC TTA AGC TCC															1056	
Val	Thr	Thr	Ala	Glu	Gly	Gly	Gln	Gly	Leu	Asn	Glu	Leu	Leu	Ser	Ser	
1040																1045
																1050
AGA AAG AGT GTA TTA AAC GGA ATT GTA AAT GGA ATT GAC ATT AAT GAT															1104	
Arg	Lys	Ser	Val	Leu	Asn	Gly	Ile	Val	Asn	Gly	Ile	Asp	Ile	Asn	Asp	
1055																1060
																1065
TGG AAC CCT GCC ACA GAC AAA TGT ATC CCC TGT CAT TAT TCT GTT GAT															1152	
Trp	Asn	Pro	Ala	Thr	Asp	Lys	Cys	Ile	Pro	Cys	His	Tyr	Ser	Val	Asp	
1070																1075
																1080
GAC CTC TCT GGA AAG GCC AAA TGT AAA GGT GCA TTG CAG AAG GAG CTG															1200	
Asp	Leu	Ser	Gly	Lys	Ala	Lys	Cys	Lys	Gly	Ala	Leu	Gln	Lys	Glu	Leu	

1085	1090	1095	
GGT TTA CCT ATA AGG CCT GAT GTT CCT CTG ATT GGC TTT ATT GGA AGG Gly Leu Pro Ile Arg Pro Asp Val Pro Leu Ile Gly Phe Ile Gly Arg 1100	1105	1110	1248
TTG GAT TAT CAG AAA GGC ATT GAT CTC ATT CAA CTT ATC ATA CCA GAT Leu Asp Tyr Gln Lys Gly Ile Asp Leu Ile Gln Leu Ile Ile Pro Asp 1120	1125	1130	1296
CTC ATG CGG GAA GAT GTT CAA TTT GTC ATG CTT GGA TCT GGT GAC CCA Leu Met Arg Glu Asp Val Gln Phe Val Met Leu Gly Ser Gly Asp Pro 1135	1140	1145	1344
GAG CTT GAA GAT TGG ATG AGA TCT ACA GAG TCG ATC TTC AAG GAT AAA Glu Leu Glu Asp Trp Met Arg Ser Thr Glu Ser Ile Phe Lys Asp Lys 1150	1155	1160	1392
TTT CGT GGA TGG GTT GGA TTT AGT GTT CCA GTT TCC CAC CGA ATA ACT Phe Arg Gly Trp Val Gly Phe Ser Val Pro Val Ser His Arg Ile Thr 1165	1170	1175	1440
GCC GGC TGC GAT ATA TTG TTA ATG CCA TCC AGA TTC GAA CCT TGT GGT Ala Gly Cys Asp Ile Leu Leu Met Pro Ser Arg Phe Glu Pro Cys Gly 1180	1185	1190	1488
CTC AAT CAG CTA TAT GCT ATG CAG TAT GGC ACA GTT CCT GTT GTC CAT Leu Asn Gln Leu Tyr Ala Met Gln Tyr Gly Thr Val Pro Val Val His 1200	1205	1210	1536
GCA ACT GGG GGC CTT AGA GAT ACC GTG GAG AAC TTC AAC CCT TTC GGT Ala Thr Gly Gly Leu Arg Asp Thr Val Glu Asn Phe Asn Pro Phe Gly 1215	1220	1225	1584
GAG AAT GGA GAG CAG GGT ACA GGG TGG GCA TTC GCA CCC CTA ACC ACA Glu Asn Gly Glu Gln Gly Thr Gly Trp Ala Phe Ala Pro Leu Thr Thr 1230	1235	1240	1632
GAA AAC ATG TTT GTG GAC ATT GCG AAC TGC AAT ATC TAC ATA CAG GGA Glu Asn Met Phe Val Asp Ile Ala Asn Cys Asn Ile Tyr Ile Gln Gly 1245	1250	1255	1680
ACA CAA GTC CTC CTG GGA AGG GCT AAT GAA GCG AGG CAT GTC AAA AGA Thr Gln Val Leu Leu Gly Arg Ala Asn Glu Ala Arg His Val Lys Arg 1260	1265	1270	1728
		1275	

CTT CAC GTG GGA CCA TGC CGC TGA
Leu His Val Gly Pro Cys Arg *
1280

1752

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Cys Val Ala Glu Leu Ser Arg Glu Gly Pro Ala Pro Arg Pro Leu Pro
1 5 10 15

Pro Ala Leu Leu Ala Pro Pro Leu Val Pro Gly Phe Leu Ala Pro Pro
20 25 30

Ala Glu Pro Thr Gly Glu Pro Ala Ser Thr Pro Pro Pro Val Pro Asp
35 40 45

Ala Gly Leu Gly Asp Leu Gly Leu Glu Pro Glu Gly Ile Ala Glu Gly
50 55 60

Ser Ile Asp Asn Thr Val Val Val Ala Ser Glu Gln Asp Ser Glu Ile
65 70 75 80

Val Val Gly Lys Glu Gln Ala Arg Ala Lys Val Thr Gln Ser Ile Val
85 90 95

Phe Val Thr Gly Glu Ala Ser Pro Tyr Ala Lys Ser Gly Leu Gly
100 105 110

Asp Val Cys Gly Ser Leu Pro Val Ala Leu Ala Ala Arg Gly His Arg
115 120 125

Val Met Val Val Met Pro Arg Tyr Leu Asn Gly Thr Ser Asp Lys Asn
130 135 140

Tyr Ala Asn Ala Phe Tyr Thr Glu Lys His Ile Arg Ile Pro Cys Phe
145 150 155 160

Gly Gly Glu His Glu Val Thr Phe Phe His Glu Tyr Arg Asp Ser Val
165 170 175

Asp Trp Val Phe Val Asp His Pro Ser Tyr His Arg Pro Gly Asn Leu
180 185 190

Tyr Gly Asp Lys Phe Gly Ala Phe Gly Asp Asn Gln Phe Arg Tyr Thr
195 200 205

Leu Leu Cys Tyr Ala Ala Cys Glu Ala Pro Leu Ile Leu Glu Leu Gly
210 215 220

Gly Tyr Ile Tyr Gly Gln Asn Cys Met Phe Val Val Asn Asp Trp His
225 230 235 240

Ala Ser Leu Val Pro Val Leu Leu Ala Ala Lys Tyr Arg Pro Tyr Gly
245 250 255

Val Tyr Lys Asp Ser Arg Ser Ile Leu Val Ile His Asn Leu Ala His
260 265 270

Gln Gly Val Glu Pro Ala Ser Thr Tyr Pro Asp Leu Gly Leu Pro Pro
275 280 285

Glu Trp Tyr Gly Ala Leu Glu Trp Val Phe Pro Glu Trp Ala Arg Arg
290 295 300

His Ala Leu Asp Lys Gly Glu Ala Val Asn Phe Leu Lys Gly Ala Val
305 310 315 320

Val Thr Ala Asp Arg Ile Val Thr Val Ser Lys Gly Tyr Ser Trp Glu
325 330 335

Val Thr Thr Ala Glu Gly Gln Gly Leu Asn Glu Leu Leu Ser Ser
340 345 350

Arg Lys Ser Val Leu Asn Gly Ile Val Asn Gly Ile Asp Ile Asn Asp
355 360 365

Trp Asn Pro Ala Thr Asp Lys Cys Ile Pro Cys His Tyr Ser Val Asp
370 375 380

Asp Leu Ser Gly Lys Ala Lys Cys Lys Gly Ala Leu Gln Lys Glu Leu
385 390 395 400

Gly Leu Pro Ile Arg Pro Asp Val Pro Leu Ile Gly Phe Ile Gly Arg
405 410 415

Leu Asp Tyr Gln Lys Gly Ile Asp Leu Ile Gln Leu Ile Ile Pro Asp
420 425 430

Leu Met Arg Glu Asp Val Gln Phe Val Met Leu Gly Ser Gly Asp Pro
435 440 445

Glu Leu Glu Asp Trp Met Arg Ser Thr Glu Ser Ile Phe Lys Asp Lys
450 455 460

Phe Arg Gly Trp Val Gly Phe Ser Val Pro Val Ser His Arg Ile Thr
465 470 475 480

Ala Gly Cys Asp Ile Leu Leu Met Pro Ser Arg Phe Glu Pro Cys Gly
485 490 495

Leu Asn Gln Leu Tyr Ala Met Gln Tyr Gly Thr Val Pro Val Val His
500 505 510

Ala Thr Gly Gly Leu Arg Asp Thr Val Glu Asn Phe Asn Pro Phe Gly
515 520 525

Glu Asn Gly Glu Gln Gly Thr Gly Trp Ala Phe Ala Pro Leu Thr Thr
530 535 540

Glu Asn Met Phe Val Asp Ile Ala Asn Cys Asn Ile Tyr Ile Gln Gly
545 550 555 560

Thr Gln Val Leu Leu Gly Arg Ala Asn Glu Ala Arg His Val Lys Arg
565 570 575

Leu His Val Gly Pro Cys Arg *
580

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2725 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Zea mays

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 91..264

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 265..2487

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 91..2490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGCCCAGAGC AGACCCGGAT TTTCGCTCTTG CGGTCGCTGG GGTTTTAGCA TTGGCTGATC	60
AGTTTCGATCC GATCCGGCTG CGAAGGGCGAG ATG GCG TTC CCG GTT TCT GGG GCG	114
Met Ala Phe Arg Val Ser Gly Ala	
-58 -55	
G TG CTC GGT GGG GCC GTA AGG GCT CCC CGA CTC ACC GGC GGC GGG GAG	162
Val Leu Gly Gly Ala Val Arg Ala Pro Arg Leu Thr Gly Gly Glu	
-50 -45 -40 -35	
GGT AGT CTA GTC TTC CCG CAC ACC GGC CTC TTC TTA ACT CGG GGT GCT	210
Gly Ser Leu Val Phe Arg His Thr Gly Leu Phe Leu Thr Arg Gly Ala	
-30 -25 -20	
CGA GTT GGA TGT TCG GGG ACG CAC GGG GCC ATG CGC GCG GCG GCC GCG	258
Arg Val Gly Cys Ser Gly Thr His Gly Ala Met Arg Ala Ala Ala	
-15 -10 -5	
GCC AGG AAG GCG GTC ATG GTT CCT GAG GGC GAG AAT GAT GGC CTC GCA	306
Ala Arg Lys Ala Val Met Val Pro Glu Gly Glu Asn Asp Gly Leu Ala	
1 5 10	
TCA AGG GCT GAC TCG GCT CAA TTC CAG TCG GAT GAA CTG GAG GTA CCA	354
Ser Arg Ala Asp Ser Ala Gln Phe Gln Ser Asp Glu Leu Glu Val Pro	
15 20 25 30	

GAC ATT TCT GAA GAG ACA ACG TGC GGT GCT GGT GTG GCT GAT GCT CAA		402
Asp Ile Ser Glu Glu Thr Thr Cys Gly Ala Gly Val Ala Asp Ala Gln		
35	40	45
 GCC TTG AAC AGA GTT CGA GTG GTC CCC CCA CCA AGC GAT GGA CAA AAA		450
Ala Leu Asn Arg Val Arg Val Val Pro Pro Pro Ser Asp Gly Gln Lys		
50	55	60
 ATA TTC CAG ATT GAC CCC ATG TTG CAA GGC TAT AAG TAC CAT CTT GAG		498
Ile Phe Gln Ile Asp Pro Met Leu Gln Gly Tyr Lys Tyr His Leu Glu		
65	70	75
 TAT CGG TAC AGC CTC TAT AGA AGA ATC CGT TCA GAC ATT GAT GAA CAT		546
Tyr Arg Tyr Ser Leu Tyr Arg Arg Ile Arg Ser Asp Ile Asp Glu His		
80	85	90
 GAA GGA GGC TTG GAA GCC TTC TCC CGT AGT TAT GAG AAG TTT GGA TTT		594
Glu Gly Gly Leu Glu Ala Phe Ser Arg Ser Tyr Glu Lys Phe Gly Phe		
95	100	105
110		
 AAT GCC AGC GCG GAA GGT ATC ACA TAT CGA GAA TGG GCT CCT GGA GCA		642
Asn Ala Ser Ala Glu Gly Ile Thr Tyr Arg Glu Trp Ala Pro Gly Ala		
115	120	125
 TTT TCT GCA GCA TTG GTG GGT GAC GTC AAC AAC TGG GAT CCA AAT GCA		690
Phe Ser Ala Ala Leu Val Gly Asp Val Asn Asn Trp Asp Pro Asn Ala		
130	135	140
 GAT CGT ATG AGC AAA AAT GAG TTT GGT GTT TGG GAA ATT TTT CTG CCT		738
Asp Arg Met Ser Lys Asn Glu Phe Gly Val Trp Glu Ile Phe Leu Pro		
145	150	155
 AAC AAT GCA GAT GGT ACA TCA CCT ATT CCT CAT GGA TCT CGT GTA AAG		786
Asn Asn Ala Asp Gly Thr Ser Pro Ile Pro His Gly Ser Arg Val Lys		
160	165	170
 GTG AGA ATG GAT ACT CCA TCA GGG ATA AAG GAT TCA ATT CCA GCC TGG		834
Val Arg Met Asp Thr Pro Ser Gly Ile Lys Asp Ser Ile Pro Ala Trp		
175	180	185
190		
 ATC AAG TAC TCA GTG CAG GCC CCA GGA GAA ATA CCA TAT GAT GGG ATT		882
Ile Lys Tyr Ser Val Gln Ala Pro Gly Glu Ile Pro Tyr Asp Gly Ile		
195	200	205
 TAT TAT GAT CCT CCT GAA GAG GTA AAG TAT GTG TTC AGG CAT GCG CAA		930

Tyr	Tyr	Asp	Pro	Pro	Glu	Glu	Val	Lys	Tyr	Val	Phe	Arg	His	Ala	Gln	
210									215							220
CCT AAA CGA CCA AAA TCA TTG CGG ATA TAT GAA ACA CAT GTC GGA ATG															978	
Pro	Lys	Arg	Pro	Lys	Ser	Leu	Arg	Ile	Tyr	Glu	Thr	His	Val	Gly	Met	
225									230							235
AGT AGC CCG GAA CCG AAG ATA AAC ACA TAT GTA AAC TTT AGG GAT GAA															1026	
Ser	Ser	Pro	Glu	Pro	Lys	Ile	Asn	Thr	Tyr	Val	Asn	Phe	Arg	Asp	Glu	
240									245							250
GTC CTC CCA AGA ATA AAA AAA CTT GGA TAC AAT GCA GTG CAA ATA ATG															1074	
Val	Leu	Pro	Arg	Ile	Lys	Lys	Leu	Gly	Tyr	Asn	Ala	Val	Gln	Ile	Met	
255									260							270
GCA ATC CAA GAG CAC TCA TAT TAT GGA AGC TTT GGA TAC CAT GTA ACT															1122	
Ala	Ile	Gln	Glu	His	Ser	Tyr	Tyr	Gly	Ser	Phe	Gly	Tyr	His	Val	Thr	
275									280							285
AAT TTT TTT GCG CCA AGT AGT CGT TTT GGT ACC CCA GAA GAT TTG AAG															1170	
Asn	Phe	Phe	Ala	Pro	Ser	Ser	Arg	Phe	Gly	Thr	Pro	Glu	Asp	Leu	Lys	
290									295							300
TCT TTG ATT GAT AGA GCA CAT GAG CTT GGT TTG CTA GTT CTC ATG GAT															1218	
Ser	Leu	Ile	Asp	Arg	Ala	His	Glu	Leu	Gly	Leu	Leu	Val	Leu	Met	Asp	
305									310							315
GTG GTT CAT AGT CAT GCG TCA AGT AAT ACT CTG GAT GGG TTG AAT GGT															1266	
Val	Val	His	Ser	His	Ala	Ser	Ser	Asn	Thr	Leu	Asp	Gly	Leu	Asn	Gly	
320									325							330
TTT GAT GGT ACA GAT ACA CAT TAC TTT CAC AGT GGT CCA CGT GGC CAT															1314	
Phe	Asp	Gly	Thr	Asp	Thr	His	Tyr	Phe	His	Ser	Gly	Pro	Arg	Gly	His	
335									340							350
CAC TGG ATG TGG GAT TCT CGC CTA TTT AAC TAT GGG AAC TGG GAA GTT															1362	
His	Trp	Met	Trp	Asp	Ser	Arg	Leu	Phe	Asn	Tyr	Gly	Asn	Trp	Glu	Val	
355									360							365
TTA AGA TTT CTT CTC TCC AAT GCT AGA TGG TGG CTC GAG GAA TAT AAG															1410	
Leu	Arg	Phe	Leu	Leu	Ser	Asn	Ala	Arg	Trp	Trp	Leu	Glu	Glu	Tyr	Lys	
370									375							380
TTT GAT GGT TTC CGT TTT GAT GGT GTG ACC TCC ATG ATG TAC ACT CAC															1458	
Phe	Asp	Gly	Phe	Arg	Phe	Asp	Gly	Val	Thr	Ser	Met	Met	Tyr	Thr	His	

385	390	395	
CAC GGA TTA CAA GTA ACA TTT ACG GGG AAC TTC AAT GAG TAT TTT GGC His Gly Leu Gln Val Thr Phe Thr Gly Asn Phe Asn Glu Tyr Phe Gly 400	405	410	1506
TTT GCC ACC GAT GTA GAT GCA GTG GTT TAC TTG ATG CTG GTA AAT GAT Phe Ala Thr Asp Val Asp Ala Val Val Tyr Leu Met Leu Val Asn Asp 415	420	425	1554
CTA ATT CAT GGA CTT TAT CCT GAG GCT GTA ACC ATT GGT GAA GAT GTT Leu Ile His Gly Leu Tyr Pro Glu Ala Val Thr Ile Gly Glu Asp Val 435	440	445	1602
AGT GGA ATG CCT ACA TTT GCC CTT CCT GTT CAC GAT GGT GGG GTA GGT Ser Gly Met Pro Thr Phe Ala Leu Pro Val His Asp Gly Gly Val Gly 450	455	460	1650
TTT GAC TAT CGG ATG CAT ATG GCT GTG GCT GAC AAA TGG ATT GAC CTT Phe Asp Tyr Arg Met His Met Ala Val Ala Asp Lys Trp Ile Asp Leu 465	470	475	1698
CTC AAG CAA AGT GAT GAA ACT TGG AAG ATG GGT GAT ATT GTG CAC ACA Leu Lys Gln Ser Asp Glu Thr Trp Lys Met Gly Asp Ile Val His Thr 480	485	490	1746
CTG ACA AAT AGG AGG TGG TTA GAG AAG TGT GTA ACT TAT GCT GAA AGT Leu Thr Asn Arg Arg Trp Leu Glu Lys Cys Val Thr Tyr Ala Glu Ser 495	500	505	1794
CAT GAT CAA GCA TTA GTC GGC GAC AAG ACT ATT GCG TTT TGG TTG ATG His Asp Gln Ala Leu Val Gly Asp Lys Thr Ile Ala Phe Trp Leu Met 515	520	525	1842
GAC AAG GAT ATG TAT GAT TTC ATG GCC CTC GAT AGA CCT TCA ACT CCT Asp Lys Asp Met Tyr Asp Phe Met Ala Leu Asp Arg Pro Ser Thr Pro 530	535	540	1890
ACC ATT GAT CGT GGG ATA GCA TTA CAT AAG ATG ATT AGA CTT ATC ACA Thr Ile Asp Arg Gly Ile Ala Leu His Lys Met Ile Arg Leu Ile Thr 545	550	555	1938
ATG GGT TTA GGA GGA GAG GGC TAT CTT AAT TTC ATG GGA AAT GAG TTT Met Gly Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu Phe 560	565	570	1986

GGA CAT CCT GAA TGG ATA GAT TTT CCA AGA GGT CCG CAA AGA CTT CCA Gly His Pro Glu Trp Ile Asp Phe Pro Arg Gly Pro Gln Arg Leu Pro	575	580	585	590	2034		
AGT GGT AAG TTT ATT CCA GGG AAT AAC AAC ACT TAT GAC AAA TGT CGT Ser Gly Lys Phe Ile Pro Gly Asn Asn Asn Ser Tyr Asp Lys Cys Arg	595		600		605	2082	
CGA AGA TTT GAC CTG GGT GAT GCA GAC TAT CTT AGG TAT CAT GGT ATG Arg Arg Phe Asp Leu Gly Asp Ala Asp Tyr Leu Arg Tyr His Gly Met	610		615		620	2130	
CAA GAG TTT GAT CAG GCA ATG CAA CAT CTT GAG CAA AAA TAT GAA TTC Gln Glu Phe Asp Gln Ala Met Gln His Leu Glu Gln Lys Tyr Glu Phe	625		630		635	2178	
ATG ACA TCT GAT CAC CAG TAT ATT TCC CGG AAA CAT GAG GAG GAT AAG Met Thr Ser Asp His Gln Tyr Ile Ser Arg Lys His Glu Glu Asp Lys	640		645		650	2226	
GTG ATT GTG TTC GAA AAG GGA GAT TTG GTA TTT GTG TTC AAC TTC CAC Val Ile Val Phe Glu Lys Gly Asp Leu Val Phe Val Phe Asn Phe His	655		660		665	670	2274
TGC AAC AAC AGC TAT TTT GAC TAC CGT ATT GGT TGT CGA AAG CCT GGG Cys Asn Asn Ser Tyr Phe Asp Tyr Arg Ile Gly Cys Arg Lys Pro Gly	675		680		685		2322
GTG TAT AAG GTG GTC TTG GAC TCC GAC GCT GGA CTA TTT GGT GGA TTT Val Tyr Lys Val Val Leu Asp Ser Asp Ala Gly Leu Phe Gly Gly Phe	690		695		700		2370
AGC AGG ATC CAT CAC GCA GCC GAG CAC TTC ACC GCC GAC TGT TCG CAT Ser Arg Ile His His Ala Ala Glu His Phe Thr Ala Asp Cys Ser His	705		710		715		2418
GAT AAT AGG CCA TAT TCA TTC TCG GTT TAT ACA CCA AGC AGA ACA TGT Asp Asn Arg Pro Tyr Ser Phe Ser Val Tyr Thr Pro Ser Arg Thr Cys	720		725		730		2466
GTC GTC TAT GCT CCA GTG GAG TGA TAGCGGGTA CTCGTTGCTG CGCGGCATGT Val Val Tyr Ala Pro Val Glu *	735		740				2520
GTGGGGCTGT CGATGTGAGG AAAAACCTTC TTCCAAAACC GGCAAGATGCA TGCATGCATG							2580

CTACAATAAG GTTCTGATAC TTTAATCGAT GCTGGAAAGC CCATGCATCT CGCTGCGTTG	2640
TCCTCTCTAT ATATATAAGA CCTTCAAGGT GTCAATTAAA CATAGAGTTT TCGTTTTTCG	2700
CTTCCCTAAA AAAAAAAA AAAAA	2725

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Ala Phe Arg Val Ser Gly Ala Val Leu Gly Gly Ala Val Arg Ala
 -58 -55 -50 -45

Pro Arg Leu Thr Gly Gly Glu Gly Ser Leu Val Phe Arg His Thr
 -40 -35 -30

Gly Leu Phe Leu Thr Arg Gly Ala Arg Val Gly Cys Ser Gly Thr His
 -25 -20 -15

Gly Ala Met Arg Ala Ala Ala Ala Arg Lys Ala Val Met Val Pro
 -10 -5 1 5

Glu Gly Glu Asn Asp Gly Leu Ala Ser Arg Ala Asp Ser Ala Gln Phe
 10 15 20

Gln Ser Asp Glu Leu Glu Val Pro Asp Ile Ser Glu Glu Thr Thr Cys
 25 30 35

Gly Ala Gly Val Ala Asp Ala Gln Ala Leu Asn Arg Val Arg Val Val
 40 45 50

Pro Pro Pro Ser Asp Gly Gln Lys Ile Phe Gln Ile Asp Pro Met Leu
 55 60 65 70

Gln Gly Tyr Lys Tyr His Leu Glu Tyr Arg Tyr Ser Leu Tyr Arg Arg
 75 80 85

Ile Arg Ser Asp Ile Asp Glu His Glu Gly Gly Leu Glu Ala Phe Ser
90 95 100

Arg Ser Tyr Glu Lys Phe Gly Phe Asn Ala Ser Ala Glu Gly Ile Thr
105 110 115

Tyr Arg Glu Trp Ala Pro Gly Ala Phe Ser Ala Ala Leu Val Gly Asp
120 125 130

Val Asn Asn Trp Asp Pro Asn Ala Asp Arg Met Ser Lys Asn Glu Phe
135 140 145 150

Gly Val Trp Glu Ile Phe Leu Pro Asn Asn Ala Asp Gly Thr Ser Pro
155 160 165

Ile Pro His Gly Ser Arg Val Lys Val Arg Met Asp Thr Pro Ser Gly
170 175 180

Ile Lys Asp Ser Ile Pro Ala Trp Ile Lys Tyr Ser Val Gln Ala Pro
185 190 195

Gly Glu Ile Pro Tyr Asp Gly Ile Tyr Tyr Asp Pro Pro Glu Glu Val
200 205 210

Lys Tyr Val Phe Arg His Ala Gln Pro Lys Arg Pro Lys Ser Leu Arg
215 220 225 230

Ile Tyr Glu Thr His Val Gly Met Ser Ser Pro Glu Pro Lys Ile Asn
235 240 245

Thr Tyr Val Asn Phe Arg Asp Glu Val Leu Pro Arg Ile Lys Lys Leu
250 255 260

Gly Tyr Asn Ala Val Gln Ile Met Ala Ile Gln Glu His Ser Tyr Tyr
265 270 275

Gly Ser Phe Gly Tyr His Val Thr Asn Phe Phe Ala Pro Ser Ser Arg
280 285 290

Phe Gly Thr Pro Glu Asp Leu Lys Ser Leu Ile Asp Arg Ala His Glu
295 300 305 310

Leu Gly Leu Leu Val Leu Met Asp Val Val His Ser His Ala Ser Ser
315 320 325

Asn Thr Leu Asp Gly Leu Asn Gly Phe Asp Gly Thr Asp Thr His Tyr
330 335 340

Phe His Ser Gly Pro Arg Gly His His Trp Met Trp Asp Ser Arg Leu
345 350 355

Phe Asn Tyr Gly Asn Trp Glu Val Leu Arg Phe Leu Leu Ser Asn Ala
360 365 370

Arg Trp Trp Leu Glu Glu Tyr Lys Phe Asp Gly Phe Arg Phe Asp Gly
375 380 385 390

Val Thr Ser Met Met Tyr Thr His His Gly Leu Gln Val Thr Phe Thr
395 400 405

Gly Asn Phe Asn Glu Tyr Phe Gly Phe Ala Thr Asp Val Asp Ala Val
410 415 420

Val Tyr Leu Met Leu Val Asn Asp Leu Ile His Gly Leu Tyr Pro Glu
425 430 435

Ala Val Thr Ile Gly Glu Asp Val Ser Gly Met Pro Thr Phe Ala Leu
440 445 450

Pro Val His Asp Gly Gly Val Gly Phe Asp Tyr Arg Met His Met Ala
455 460 465 470

Val Ala Asp Lys Trp Ile Asp Leu Leu Lys Gln Ser Asp Glu Thr Trp
475 480 485

Lys Met Gly Asp Ile Val His Thr Leu Thr Asn Arg Arg Trp Leu Glu
490 495 500

Lys Cys Val Thr Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly Asp
505 510 515

Lys Thr Ile Ala Phe Trp Leu Met Asp Lys Asp Met Tyr Asp Phe Met
520 525 530

Ala Leu Asp Arg Pro Ser Thr Pro Thr Ile Asp Arg Gly Ile Ala Leu
535 540 545 550

His Lys Met Ile Arg Leu Ile Thr Met Gly Leu Gly Gly Glu Gly Tyr
555 560 565

Leu Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe
 570 575 580

 Pro Arg Gly Pro Gln Arg Leu Pro Ser Gly Lys Phe Ile Pro Gly Asn
 585 590 595

 Asn Asn Ser Tyr Asp Lys Cys Arg Arg Arg Phe Asp Leu Gly Asp Ala
 600 605 610

 Asp Tyr Leu Arg Tyr His Gly Met Gln Glu Phe Asp Gln Ala Met Gln
 615 620 625 630

 His Leu Glu Gln Lys Tyr Glu Phe Met Thr Ser Asp His Gln Tyr Ile
 635 640 645

 Ser Arg Lys His Glu Glu Asp Lys Val Ile Val Phe Glu Lys Gly Asp
 650 655 660

 Leu Val Phe Val Phe Asn Phe His Cys Asn Asn Ser Tyr Phe Asp Tyr
 665 670 675

 Arg Ile Gly Cys Arg Lys Pro Gly Val Tyr Lys Val Val Leu Asp Ser
 680 685 690

 Asp Ala Gly Leu Phe Gly Phe Ser Arg Ile His His Ala Ala Glu
 695 700 705 710

 His Phe Thr Ala Asp Cys Ser His Asp Asn Arg Pro Tyr Ser Phe Ser
 715 720 725

 Val Tyr Thr Pro Ser Arg Thr Cys Val Val Tyr Ala Pro Val Glu *
 730 735 740

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2763 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Zea mays

(ix) FEATURE:

(A) NAME/KEY: transit_peptide

(B) LOCATION: 2..190

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 191..2467

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..2470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

G CTG TGC CTC GTG TCG CCC TCT TCC TCG CCG ACT CCG CTT CCG CCG	46
Leu Cys Leu Val Ser Pro Ser Ser Pro Thr Pro Leu Pro Pro	
-63 -60 -55 -50	
CCG CGG CGC TCT CGC TCG CAT GCT GAT CGG GCG GCA CCG CCG GGG ATC	94
Pro Arg Arg Ser Arg Ser His Ala Asp Arg Ala Ala Pro Pro Gly Ile	
-45 -40 -35	
GCG GGT GGC GGC AAT GTG CGC CTG AGT GTG TTG TCT GTC CAG TGC AAG	142
Ala Gly Gly Asn Val Arg Leu Ser Val Leu Ser Val Gln Cys Lys	
-30 -25 -20	
GCT CGC CGG TCA GGG GTG CGG AAG GTC AAG AGC AAA TTC GCC ACT GCA	190
Ala Arg Arg Ser Gly Val Arg Lys Val Lys Ser Lys Phe Ala Thr Ala	
-15 -10 -5	
GCT ACT GTG CAA GAA GAT AAA ACT ATG GCA ACT GCC AAA GGC GAT GTC	238
Ala Thr Val Gln Glu Asp Lys Thr Met Ala Thr Ala Lys Gly Asp Val	
1 5 10 15	
GAC CAT CTC CCC ATA TAC GAC CTG GAC CCC AAG CTG GAG ATA TTC AAG	286
Asp His Leu Pro Ile Tyr Asp Leu Asp Pro Lys Leu Glu Ile Phe Lys	
20 25 30	
GAC CAT TTC AGG TAC CGG ATG AAA AGA TTC CTA GAG CAG AAA GGA TCA	334
Asp His Phe Arg Tyr Arg Met Lys Arg Phe Leu Glu Gln Lys Gly Ser	
35 40 45	

ATT GAA GAA AAT GAG GGA AGT CTT GAA TCT TTT TCT AAA GGC TAT TTG Ile Glu Glu Asn Glu Gly Ser Leu Glu Ser Phe Ser Lys Gly Tyr Leu	50	55	60	382	
AAA TTT GGG ATT AAT ACA AAT GAG GAT GGA ACT GTA TAT CGT GAA TGG Lys Phe Gly Ile Asn Thr Asn Glu Asp Gly Thr Val Tyr Arg Glu Trp	65	70	75	80	430
GCA CCT GCT GCG CAG GAG GCA GAG CTT ATT GGT GAC TTC AAT GAC TGG Ala Pro Ala Ala Gln Glu Ala Glu Leu Ile Gly Asp Phe Asn Asp Trp	85	90	95		478
AAT GGT GCA AAC CAT AAG ATG GAG AAG GAT AAA TTT GGT GTT TGG TCG Asn Gly Ala Asn His Lys Met Glu Lys Asp Lys Phe Gly Val Trp Ser	100	105	110		526
ATC AAA ATT GAC CAT GTC AAA GGG AAA CCT GCC ATC CCT CAC AAT TCC Ile Lys Ile Asp His Val Lys Gly Lys Pro Ala Ile Pro His Asn Ser	115	120	125		574
AAG GTT AAA TTT CGC TTT CTA CAT GGT GGA GTA TGG GTT GAT CGT ATT Lys Val Lys Phe Arg Phe Leu His Gly Gly Val Trp Val Asp Arg Ile	130	135	140		622
CCA GCA TTG ATT CGT TAT GCG ACT GTT GAT GCC TCT AAA TTT GGA GCT Pro Ala Leu Ile Arg Tyr Ala Thr Val Asp Ala Ser Lys Phe Gly Ala	145	150	155	160	670
CCC TAT GAT GGT GTT CAT TGG GAT CCT CCT GCT TCT GAA AGG TAC ACA Pro Tyr Asp Gly Val His Trp Asp Pro Pro Ala Ser Glu Arg Tyr Thr	165	170	175		718
TTT AAG CAT CCT CGG CCT TCA AAG CCT GCT GCT CCA CGT ATC TAT GAA Phe Lys His Pro Arg Pro Ser Lys Pro Ala Ala Pro Arg Ile Tyr Glu	180	185	190		766
GCC CAT GTA GGT ATG AGT GGT GAA AAG CCA GCA GTA AGC ACA TAT AGG Ala His Val Gly Met Ser Gly Glu Lys Pro Ala Val Ser Thr Tyr Arg	195	200	205		814
GAA TTT GCA GAC AAT GTG TTG CCA CGC ATA CGA GCA AAT AAC TAC AAC Glu Phe Ala Asp Asn Val Leu Pro Arg Ile Arg Ala Asn Asn Tyr Asn	210	215	220		862
ACA GTT CAG TTG ATG GCA GTT ATG GAG CAT TCG TAC TAT GCT TCT TTC					910

Thr Val Gln Leu Met Ala Val Met Glu His Ser Tyr Tyr Ala Ser Phe				
225	230	235	240	
GGG TAC CAT GTG ACA AAT TTC TTT GCG GTT AGC AGC AGA TCA GGC ACA				958
Gly Tyr His Val Thr Asn Phe Phe Ala Val Ser Ser Arg Ser Gly Thr				
245	250	255		
CCA GAG GAC CTC AAA TAT CTT GTT GAT AAG GCA CAC AGT TTG GGT TTG				1006
Pro Glu Asp Leu Lys Tyr Leu Val Asp Lys Ala His Ser Leu Gly Leu				
260	265	270		
CGA GTT CTG ATG GAT GTT GTC CAT AGC CAT GCA AGT AAT AAT GTC ACA				1054
Arg Val Leu Met Asp Val Val His Ser His Ala Ser Asn Asn Val Thr				
275	280	285		
GAT GGT TTA AAT GGC TAT GAT GTT GGA CAA AGC ACC CAA GAG TCC TAT				1102
Asp Gly Leu Asn Gly Tyr Asp Val Gly Gln Ser Thr Gln Glu Ser Tyr				
290	295	300		
TTT CAT GCG GGA GAT AGA GGT TAT CAT AAA CTT TGG GAT AGT CGG CTG				1150
Phe His Ala Gly Asp Arg Gly Tyr His Lys Leu Trp Asp Ser Arg Leu				
305	310	315	320	
TTC AAC TAT GCT AAC TGG GAG GTA TTA AGG TTT CTT CTT TCT AAC CTG				1198
Phe Asn Tyr Ala Asn Trp Glu Val Leu Arg Phe Leu Leu Ser Asn Leu				
325	330	335		
AGA TAT TGG TTG GAT GAA TTC ATG TTT GAT GGC TTC CGA TTT GAT GGA				1246
Arg Tyr Trp Leu Asp Glu Phe Met Phe Asp Gly Phe Arg Phe Asp Gly				
340	345	350		
GTT ACA TCA ATG CTG TAT CAT CAC CAT GGT ATC AAT GTG GGG TTT ACT				1294
Val Thr Ser Met Leu Tyr His His His Gly Ile Asn Val Gly Phe Thr				
355	360	365		
GGA AAC TAC CAG GAA TAT TTC AGT TTG GAC ACA GCT GTG GAT GCA GTT				1342
Gly Asn Tyr Gln Glu Tyr Phe Ser Leu Asp Thr Ala Val Asp Ala Val				
370	375	380		
GTT TAC ATG ATG CTT GCA AAC CAT TTA ATG CAC AAA CTC TTG CCA GAA				1390
Val Tyr Met Met Leu Ala Asn His Leu Met His Lys Leu Leu Pro Glu				
385	390	395	400	
GCA ACT GTT GTT GCT GAA GAT GTT TCA GGC ATG CCG GTC CTT TGC CGG				1438
Ala Thr Val Val Ala Glu Asp Val Ser Gly Met Pro Val Leu Cys Arg				

405	410	415	
CCA GTT GAT GAA GGT GGG GTT GGG TTT GAC TAT CGC CTG GCA ATG GCT Pro Val Asp Glu Gly Gly Val Gly Phe Asp Tyr Arg Leu Ala Met Ala			1486
420	425	430	
ATC CCT GAT AGA TGG ATT GAC TAC CTG AAG AAT AAA GAT GAC TCT GAG Ile Pro Asp Arg Trp Ile Asp Tyr Leu Lys Asn Lys Asp Asp Ser Glu			1534
435	440	445	
TGG TCG ATG GGT GAA ATA GCG CAT ACT TTG ACT AAC AGG AGA TAT ACT Trp Ser Met Gly Glu Ile Ala His Thr Leu Thr Asn Arg Arg Tyr Thr			1582
450	455	460	
GAA AAA TGC ATC GCA TAT GCT GAG AGC CAT GAT CAG TCT ATT GTT GGC Glu Lys Cys Ile Ala Tyr Ala Glu Ser His Asp Gln Ser Ile Val Gly			1630
465	470	475	480
GAC AAA ACT ATT GCA TTT CTC CTG ATG GAC AAG GAA ATG TAC ACT GGC Asp Lys Thr Ile Ala Phe Leu Leu Met Asp Lys Glu Met Tyr Thr Gly			1678
485	490	495	
ATG TCA GAC TTG CAG CCT GCT TCA CCT ACA ATT GAT CGA GGG ATT GCA Met Ser Asp Leu Gln Pro Ala Ser Pro Thr Ile Asp Arg Gly Ile Ala			1726
500	505	510	
CTC CAA AAG ATG ATT CAC TTC ATC ACA ATG GCC CTT GGA GGT GAT GGC Leu Gln Lys Met Ile His Phe Ile Thr Met Ala Leu Gly Gly Asp Gly			1774
515	520	525	
TAC TTG AAT TTT ATG GGA AAT GAG TTT GGT CAC CCA GAA TGG ATT GAC Tyr Leu Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp			1822
530	535	540	
TTT CCA AGA GAA GGG AAC AAC TGG AGC TAT GAT AAA TGC AGA CGA CAG Phe Pro Arg Glu Gly Asn Asn Trp Ser Tyr Asp Lys Cys Arg Arg Gln			1870
545	550	555	560
TGG AGC CTT GTG GAC ACT GAT CAC TTG CGG TAC AAG TAC ATG AAT GCG Trp Ser Leu Val Asp Thr Asp His Leu Arg Tyr Lys Tyr Met Asn Ala			1918
565	570	575	
TTT GAC CAA GCG ATG AAT GCG CTC GAT GAG AGA TTT TCC TTC CTT TCG Phe Asp Gln Ala Met Asn Ala Leu Asp Glu Arg Phe Ser Phe Leu Ser			1966
580	585	590	

TCG TCA AAG CAG ATC GTC AGC GAC ATG AAC GAT GAG GAA AAG GTT ATT Ser Ser Lys Gln Ile Val Ser Asp Met Asn Asp Glu Glu Lys Val Ile 595 600 605	2014
 GTC TTT GAA CGT GGA GAT TTA GTT TTT GTT TTC AAT TTC CAT CCC AAG Val Phe Glu Arg Gly Asp Leu Val Phe Val Phe Asn Phe His Pro Lys 610 615 620	2062
 AAA ACT TAC GAG GGC TAC AAA GTG GGA TGC GAT TTG CCT GGG AAA TAC Lys Thr Tyr Glu Gly Tyr Lys Val Gly Cys Asp Leu Pro Gly Lys Tyr 625 630 635 640	2110
 AGA GTA GCC CTG GAC TCT GAT GCT CTG GTC TTC GGT GGA CAT GGA AGA Arg Val Ala Leu Asp Ser Asp Ala Leu Val Phe Gly Gly His Gly Arg 645 650 655	2158
 GTT GGC CAC GAC GTG GAT CAC TTC ACG TCG CCT GAA GGG GTG CCA GGG Val Gly His Asp Val Asp His Phe Thr Ser Pro Glu Gly Val Pro Gly 660 665 670	2206
 GTG CCC GAA ACG AAC TTC AAC AAC CGG CCG AAC TCG TTC AAA GTC CTT Val Pro Glu Thr Asn Phe Asn Asn Arg Pro Asn Ser Phe Lys Val Leu 675 680 685	2254
 TCT CCG CCC CGC ACC TGT GTG GCT TAT TAC CGT GTA GAC GAA GCA GGG Ser Pro Pro Arg Thr Cys Val Ala Tyr Tyr Arg Val Asp Glu Ala Gly 690 695 700	2302
 GCT GGA CGA CGT CTT CAC GCG AAA GCA GAG ACA GGA AAG ACG TCT CCA Ala Gly Arg Arg Leu His Ala Lys Ala Glu Thr Gly Lys Thr Ser Pro 705 710 715 720	2350
 GCA GAG AGC ATC GAC GTC AAA GCT TCC AGA GCT AGT AGC AAA GAA GAC Ala Glu Ser Ile Asp Val Lys Ala Ser Arg Ala Ser Ser Lys Glu Asp 725 730 735	2398
 AAG GAG GCA ACG GCT GGT GGC AAG AAG GGA TGG AAG TTT GCG CGG CAG Lys Glu Ala Thr Ala Gly Gly Lys Lys Gly Trp Lys Phe Ala Arg Gln 740 745 750	2446
 CCA TCC GAT CAA GAT ACC AAA TGA AGCCACGAGT CCTTGGTGAG GACTGGACTG Pro Ser Asp Gln Asp Thr Lys *	2500
755 760	
 GCTGCCGGCG CCCTGTTAGT AGTCCTGCTC TACTGGACTA GCCGCCGCTG GCGCCCTTGG	2560

AACGGTCCTT TCCTGTAGCT TGCAGGCGAC TGGTGTCTCA TCACCGAGCA GGCAGGCACT	2620
GCTTGTATAG CTTTCTAGA ATAATAATCA GGGATGGATG GATGGTGTGT ATTGGCTATC	2680
TGGCTAGACG TGCATGTGCC CAGTTGTAT GTACAGGAGC AGTTCCCGTC CAGAATAAAA	2740
AAAAACTTGT TGGGGGGTTT TTC	2763

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 823 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Leu Cys Leu Val Ser Pro Ser Ser Ser Pro Thr Pro Leu Pro Pro Pro
 -63 -60 -55 -50

Arg Arg Ser Arg Ser His Ala Asp Arg Ala Ala Pro Pro Gly Ile Ala
 -45 -40 -35

Gly Gly Gly Asn Val Arg Leu Ser Val Leu Ser Val Gln Cys Lys Ala
 -30 -25 -20

Arg Arg Ser Gly Val Arg Lys Val Lys Ser Lys Phe Ala Thr Ala Ala
 -15 -10 -5 1

Thr Val Gln Glu Asp Lys Thr Met Ala Thr Ala Lys Gly Asp Val Asp
 5 10 15

His Leu Pro Ile Tyr Asp Leu Asp Pro Lys Leu Glu Ile Phe Lys Asp
 20 25 30

His Phe Arg Tyr Arg Met Lys Arg Phe Leu Glu Gln Lys Gly Ser Ile
 35 40 45

Glu Glu Asn Glu Gly Ser Leu Glu Ser Phe Ser Lys Gly Tyr Leu Lys
 50 55 60 65

Phe Gly Ile Asn Thr Asn Glu Asp Gly Thr Val Tyr Arg Glu Trp Ala

70

75

80

Gly Ala Asn His Lys Met Glu Lys Asp Lys Phe Gly Val Trp Ser Ile
100 105 110

Lys Ile Asp His Val Lys Gly Lys Pro Ala Ile Pro His Asn Ser Lys
 115 120 125

Val Lys Phe Arg Phe Leu His Gly Gly Val Trp Val Asp Arg Ile Pro
130 135 140 145

Ala Leu Ile Arg Tyr Ala Thr Val Asp Ala Ser Lys Phe Gly Ala Pro
150 155 160

Tyr Asp Gly Val His Trp Asp Pro Pro Ala Ser Glu Arg Tyr Thr Phe
165 170 175

Lys His Pro Arg Pro Ser Lys Pro Ala Ala Pro Arg Ile Tyr Glu Ala
180 185 190

His Val Gly Met Ser Gly Glu Lys Pro Ala Val Ser Thr Tyr Arg Glu
195 200 205

Phe Ala Asp Asn Val Leu Pro Arg Ile Arg Ala Asn Asn Tyr Asn Thr
 210 215 220 225

Val Gln Leu Met Ala Val Met Glu His Ser Tyr Tyr Ala Ser Phe Gly
230 235 240

Tyr His Val Thr Asn Phe Phe Ala Val Ser Ser Arg Ser Gly Thr Pro

245 250 255

Glu Asp Leu Lys Tyr Leu Val Asp Lys Ala His Ser Leu Gly Leu Arg
260 265 270

Val Leu Met Asp Val Val His Ser His Ala Ser Asn Asn Val Thr Asp
275 280 285

Gly Leu Asn Gly Tyr Asp Val Gly Gln Ser Thr Gln Glu Ser Tyr Phe
290 295 300 305

His Ala Gly Asp Arg Gly Tyr His Lys Leu Trp Asp Ser Arg Leu Phe

	310	315	320
Asn Tyr Ala Asn Trp Glu Val Leu Arg Phe Leu Leu Ser Asn Leu Arg			
325	330	335	
Tyr Trp Leu Asp Glu Phe Met Phe Asp Gly Phe Arg Phe Asp Gly Val			
340	345	350	
Thr Ser Met Leu Tyr His His His Gly Ile Asn Val Gly Phe Thr Gly			
355	360	365	
Asn Tyr Gln Glu Tyr Phe Ser Leu Asp Thr Ala Val Asp Ala Val Val			
370	375	380	385
Tyr Met Met Leu Ala Asn His Leu Met His Lys Leu Leu Pro Glu Ala			
390	395	400	
Thr Val Val Ala Glu Asp Val Ser Gly Met Pro Val Leu Cys Arg Pro			
405	410	415	
Val Asp Glu Gly Val Gly Phe Asp Tyr Arg Leu Ala Met Ala Ile			
420	425	430	
Pro Asp Arg Trp Ile Asp Tyr Leu Lys Asn Lys Asp Asp Ser Glu Trp			
435	440	445	
Ser Met Gly Glu Ile Ala His Thr Leu Thr Asn Arg Arg Tyr Thr Glu			
450	455	460	465
Lys Cys Ile Ala Tyr Ala Glu Ser His Asp Gln Ser Ile Val Gly Asp			
470	475	480	
Lys Thr Ile Ala Phe Leu Leu Met Asp Lys Glu Met Tyr Thr Gly Met			
485	490	495	
Ser Asp Leu Gln Pro Ala Ser Pro Thr Ile Asp Arg Gly Ile Ala Leu			
500	505	510	
Gln Lys Met Ile His Phe Ile Thr Met Ala Leu Gly Gly Asp Gly Tyr			
515	520	525	
Leu Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe			
530	535	540	545
Pro Arg Glu Gly Asn Asn Trp Ser Tyr Asp Lys Cys Arg Arg Gln Trp			

550	555	560
Ser Leu Val Asp Thr Asp His Leu Arg Tyr Lys Tyr Met Asn Ala Phe		
565	570	575
Asp Gln Ala Met Asn Ala Leu Asp Glu Arg Phe Ser Phe Leu Ser Ser		
580	585	590
Ser Lys Gln Ile Val Ser Asp Met Asn Asp Glu Glu Lys Val Ile Val		
595	600	605
Phe Glu Arg Gly Asp Leu Val Phe Val Phe Asn Phe His Pro Lys Lys		
610	615	620
Thr Tyr Glu Gly Tyr Lys Val Gly Cys Asp Leu Pro Gly Lys Tyr Arg		
630	635	640
Val Ala Leu Asp Ser Asp Ala Leu Val Phe Gly Gly His Gly Arg Val		
645	650	655
Gly His Asp Val Asp His Phe Thr Ser Pro Glu Gly Val Pro Gly Val		
660	665	670
Pro Glu Thr Asn Phe Asn Asn Arg Pro Asn Ser Phe Lys Val Leu Ser		
675	680	685
Pro Pro Arg Thr Cys Val Ala Tyr Tyr Arg Val Asp Glu Ala Gly Ala		
690	695	700
Gly Arg Arg Leu His Ala Lys Ala Glu Thr Gly Lys Thr Ser Pro Ala		
710	715	720
Glu Ser Ile Asp Val Lys Ala Ser Arg Ala Ser Ser Lys Glu Asp Lys		
725	730	735
Glu Ala Thr Ala Gly Gly Lys Gly Trp Lys Phe Ala Arg Gln Pro		
740	745	750
Ser Asp Gln Asp Thr Lys *		
755	760	

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Zea mays

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATG GCG ACG CCC TCG GCC GTG GGC GCC GCG TGC CTC CTC CTC GCG CGG	48
Met Ala Thr Pro Ser Ala Val Gly Ala Ala Cys Leu Leu Leu Ala Arg	
765 770 775	

GCC GCC TGG CCG GCC GCC GTC GGC GAC CGG GCG CGC CCG CGG AGG CTC	96
Ala Ala Trp Pro Ala Ala Val Gly Asp Arg Ala Arg Pro Arg Arg Leu	
780 785 790	

CAG CGC GTG CTG CGC CGC CGG TGC GTC GCG GAG CTG AGC AGG GAG GGG	144
Gln Arg Val Leu Arg Arg Arg Cys Val Ala Glu Leu Ser Arg Glu Gly	
795 800 805	

CCC CAT ATG	153
Pro His Met	
810	

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Ala Thr Pro Ser Ala Val Gly Ala Ala Cys Leu Leu Leu Ala Arg
1 5 10 15

Ala Ala Trp Pro Ala Ala Val Gly Asp Arg Ala Arg Pro Arg Arg Leu
20 25 30

Gln Arg Val Leu Arg Arg Arg Cys Val Ala Glu Leu Ser Arg Glu Gly
35 40 45

Pro His Met
50

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGC GTC GCG GAG CTG AGC AGG GAG GAC CTC GGT CTC GAA CCT GAA GGG 48
Cys Val Ala Glu Leu Ser Arg Glu Asp Leu Gly Leu Glu Pro Glu Gly
55 60 65

ATT GCT GAA GGT TCC ATC GAT AAC ACA GTA GTT GTG GCA AGT GAG CAA 96
Ile Ala Glu Gly Ser Ile Asp Asn Thr Val Val Ala Ser Glu Gln
70 75 80

GAT TCT GAG ATT GTG GTT GGA AAG GAG CAA GCT CGA GCT AAA GTA ACA 144
Asp Ser Glu Ile Val Val Gly Lys Glu Gln Ala Arg Ala Lys Val Thr
85 90 95

CAA AGC ATT GTC TTT GTA ACC GGC GAA GCT TCT CCT TAT GCA ARG TCT 192

Gln Ser Ile Val Phe Val Thr Gly Glu Ala Ser Pro Tyr Ala Lys Ser				
100	105	110	115	
GGG GGT CTA GGA GAT GTT TGT GGT TCA TTG CCA GTT GCT CTT GCT GCT				240
Gly Gly Leu Gly Asp Val Cys Gly Ser Leu Pro Val Ala Leu Ala Ala				
120	125	130		
CGT GGT CAC CGT GTG ATG GTT GTA ATG CCC AGA TAT TTA AAT GGT ACC				288
Arg Gly His Arg Val Met Val Val Met Pro Arg Tyr Leu Asn Gly Thr				
135	140	145		
TCC GAT AAG AAT TAT GCA AAT GCA TTT TAC ACA CAA AAA CAC ATT CGG				336
Ser Asp Lys Asn Tyr Ala Asn Ala Phe Tyr Thr Glu Lys His Ile Arg				
150	155	160		
ATT CCA TGC TTT GGC GGT GAA CAT GAA GTT ACC TTC TTC CAT GAG TAT				384
Ile Pro Cys Phe Gly Gly Glu His Glu Val Thr Phe Phe His Glu Tyr				
165	170	175		
AGA GAT TCA GTT GAC TGG GTG TTT GTT GAT CAT CCC TCA TAT CAC AGA				432
Arg Asp Ser Val Asp Trp Val Phe Val Asp His Pro Ser Tyr His Arg				
180	185	190	195	
CCT GGA AAT TTA TAT GGA GAT AAG TTT GGT GCT TTT GGT GAT AAT CAG				480
Pro Gly Asn Leu Tyr Gly Asp Lys Phe Gly Ala Phe Gly Asp Asn Gln				
200	205	210		
TTC AGA TAC ACA CTC CTT TGC TAT GCT GCA TGT GAG GCT CCT TTG ATC				528
Phe Arg Tyr Thr Leu Leu Cys Tyr Ala Ala Cys Glu Ala Pro Leu Ile				
215	220	225		
CTT GAA TTG GGA GGA TAT ATT TAT GGA CAG AAT TGC ATG TTT GTT GTC				576
Leu Glu Leu Gly Gly Tyr Ile Tyr Gly Gln Asn Cys Met Phe Val Val				
230	235	240		
AAT GAT TGG CAT GCC AGT CTA GTG CCA GTC CTT CTT GCT GCA AAA TAT				624
Asn Asp Trp His Ala Ser Leu Val Pro Val Leu Leu Ala Ala Lys Tyr				
245	250	255		
AGA CCA TAT GGT GTT TAT AAA GAC TCC CGC AGC ATT CTT GTA ATA CAT				672
Arg Pro Tyr Gly Val Tyr Lys Asp Ser Arg Ser Ile Leu Val Ile His				
260	265	270	275	
AAT TTA GCA CAT CAG GGT GTA GAG CCT GCA ACC ACA TAT CCT GAC CTT				720
Asn Leu Ala His Gln Gly Val Glu Pro Ala Ser Thr Tyr Pro Asp Leu				

280	285	290	
GGG TTG CCA CCT GAA TGG TAT GGA GCT CTG GAG TGG GTA TTC CCT GAA Gly Leu Pro Pro Glu Trp Tyr Gly Ala Leu Glu Trp Val Phe Pro Glu			768
295	300	305	
TGG GCG AGG AGG CAT GCC CTT GAC AAG GGT GAG GCA GTT AAT TTT TTG Trp Ala Arg Arg His Ala Leu Asp Lys Gly Glu Ala Val Asn Phe Leu			816
310	315	320	
AAA GGT GCA GTT GTG ACA GCA GAT CGA ATC GTG ACT GTC AGT AAG GGT Lys Gly Ala Val Val Thr Ala Asp Arg Ile Val Thr Val Ser Lys Gly			864
325	330	335	
TAT TCG TGG GAG GTC ACA ACT GCT GAA GGT GGA CAG GGC CTC AAT GAG Tyr Ser Trp Glu Val Thr Thr Ala Glu Gly Gly Gln Gly Leu Asn Glu			912
340	345	350	355
CTC TTA AGC TCC AGA AAG AGT GTA TTA AAC GGA ATT GTA AAT GGA ATT Leu Leu Ser Ser Arg Lys Ser Val Leu Asn Gly Ile Val Asn Gly Ile			960
360	365	370	
GAC ATT AAT GAT TGG AAC CCT GCC ACA GAC AAA TGT ATC CCC TGT CAT Asp Ile Asn Asp Trp Asn Pro Ala Thr Asp Lys Cys Ile Pro Cys His			1008
375	380	385	
TAT TCT GTT GAT GAC CTC TCT GGA AAG GCC AAA TGT AAA GGT GCA TTG Tyr Ser Val Asp Asp Leu Ser Gly Lys Ala Lys Cys Lys Gly Ala Leu			1056
390	395	400	
CAG AAG GAG CTG GGT TTA CCT ATA AGG CCT GAT GTT CCT CTG ATT GGC Gln Lys Glu Leu Gly Leu Pro Ile Arg Pro Asp Val Pro Leu Ile Gly			1104
405	410	415	
TTT ATT GGA AGG TTG GAT TAT CAG AAA GGC ATT GAT CTC ATT CAA CTT Phe Ile Gly Arg Leu Asp Tyr Gln Lys Gly Ile Asp Leu Ile Gln Leu			1152
420	425	430	435
ATC ATA CCA GAT CTC ATG CGG GAA GAT GTT CAA TTT GTC ATG CTT GGA Ile Ile Pro Asp Leu Met Arg Glu Asp Val Gln Phe Val Met Leu Gly			1200
440	445	450	
TCT GGT GAC CCA GAG CTT GAA GAT TGG ATG AGA TCT ACA GAG TCG ATC Ser Gly Asp Pro Glu Leu Glu Asp Trp Met Arg Ser Thr Glu Ser Ile			1248
455	460	465	

TTC AAG GAT AAA TTT CGT GGA TGG GTT GGA TTT AGT GTT CCA GTT TCC		1296
Phe Lys Asp Lys Phe Arg Gly Trp Val Gly Phe Ser Val Pro Val Ser		
470	475	480
CAC CGA ATA ACT GCC GGC TGC GAT ATA TTG TTA ATG CCA TCC AGA TTC		1344
His Arg Ile Thr Ala Gly Cys Asp Ile Leu Leu Met Pro Ser Arg Phe		
485	490	495
GAA CCT TGT GGT CTC AAT CAG CTA TAT GCT ATG CAG TAT GGC ACA GTT		1392
Glu Pro Cys Gly Leu Asn Gln Leu Tyr Ala Met Gln Tyr Gly Thr Val		
500	505	510
515		
CCT GTT GTC CAT GCA ACT GGG GGC CTT AGA GAT ACC GTG GAG AAC TTC		1440
Pro Val Val His Ala Thr Gly Leu Arg Asp Thr Val Glu Asn Phe		
520	525	530
AAC CCT TTC GGT GAG AAT GGA GAG CAG GGT ACA GGG TGG GCA TTC GCA		1488
Asn Pro Phe Gly Glu Asn Gly Glu Gln Gly Thr Gly Trp Ala Phe Ala		
535	540	545
CCC CTA ACC ACA GAA AAC ATG TTT GTG GAC ATT GCG AAC TGC AAT ATC		1536
Pro Leu Thr Thr Glu Asn Met Phe Val Asp Ile Ala Asn Cys Asn Ile		
550	555	560
TAC ATA CAG GGA ACA CAA GTC CTC CTG GGA AGG GCT AAT GAA GCG AGG		1584
Tyr Ile Gln Gly Thr Gln Val Leu Leu Gly Arg Ala Asn Glu Ala Arg		
565	570	575
CAT GTC AAA AGA CTT CAC GTG GGA CCA TGC CGC TGA		1620
His Val Lys Arg Leu His Val Gly Pro Cys Arg *		
580	585	590

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Cys Val Ala Glu Leu Ser Arg Glu Asp Leu Gly Leu Glu Pro Glu Gly

1	5	10	15
Ile Ala Gln Gly Ser Ile Asp Asn Thr Val Val Val Ala Ser Glu Gln			
20	25	30	
Asp Ser Glu Ile Val Val Gly Lys Glu Gln Ala Arg Ala Lys Val Thr			
35	40	45	
Gln Ser Ile Val Phe Val Thr Gly Glu Ala Ser Pro Tyr Ala Lys Ser			
50	55	60	
Gly Gly Leu Gly Asp Val Cys Gly Ser Leu Pro Val Ala Leu Ala Ala			
65	70	75	80
Arg Gly His Arg Val Met Val Val Met Pro Arg Tyr Leu Asn Gly Thr			
85	90	95	
Ser Asp Lys Asn Tyr Ala Asn Ala Phe Tyr Thr Glu Lys His Ile Arg			
100	105	110	
Ile Pro Cys Phe Gly Gly Glu His Glu Val Thr Phe Phe His Glu Tyr			
115	120	125	
Arg Asp Ser Val Asp Trp Val Phe Val Asp His Pro Ser Tyr His Arg			
130	135	140	
Pro Gly Asn Leu Tyr Gly Asp Lys Phe Gly Ala Phe Gly Asp Asn Gln			
145	150	155	160
Phe Arg Tyr Thr Leu Leu Cys Tyr Ala Ala Cys Glu Ala Pro Leu Ile			
165	170	175	
Leu Glu Leu Gly Gly Tyr Ile Tyr Gly Gln Asn Cys Met Phe Val Val			
180	185	190	
Asn Asp Trp His Ala Ser Leu Val Pro Val Leu Leu Ala Ala Lys Tyr			
195	200	205	
Arg Pro Tyr Gly Val Tyr Lys Asp Ser Arg Ser Ile Leu Val Ile His			
210	215	220	
Asn Leu Ala His Gln Gly Val Glu Pro Ala Ser Thr Tyr Pro Asp Leu			
225	230	235	240
Gly Leu Pro Pro Glu Trp Tyr Gly Ala Leu Glu Trp Val Phe Pro Glu			

	245	250	255
Trp Ala Arg Arg His Ala Leu Asp Lys Gly Glu Ala Val Asn Phe Leu			
260	265	270	
Lys Gly Ala Val Val Thr Ala Asp Arg Ile Val Thr Val Ser Lys Gly			
275	280	285	
Tyr Ser Trp Glu Val Thr Thr Ala Glu Gly Gly Gln Gly Leu Asn Glu			
290	295	300	
Leu Leu Ser Ser Arg Lys Ser Val Leu Asn Gly Ile Val Asn Gly Ile			
305	310	315	320
Asp Ile Asn Asp Trp Asn Pro Ala Thr Asp Lys Cys Ile Pro Cys His			
325	330	335	
Tyr Ser Val Asp Asp Leu Ser Gly Lys Ala Lys Cys Lys Gly Ala Leu			
340	345	350	
Gln Lys Glu Leu Gly Leu Pro Ile Arg Pro Asp Val Pro Leu Ile Gly			
355	360	365	
Phe Ile Gly Arg Leu Asp Tyr Gln Lys Gly Ile Asp Leu Ile Gln Leu			
370	375	380	
Ile Ile Pro Asp Leu Met Arg Glu Asp Val Gln Phe Val Met Leu Gly			
385	390	395	400
Ser Gly Asp Pro Glu Leu Glu Asp Trp Met Arg Ser Thr Glu Ser Ile			
405	410	415	
Phe Lys Asp Lys Phe Arg Gly Trp Val Gly Phe Ser Val Pro Val Ser			
420	425	430	
His Arg Ile Thr Ala Gly Cys Asp Ile Leu Leu Met Pro Ser Arg Phe			
435	440	445	
Glu Pro Cys Gly Leu Asn Gln Leu Tyr Ala Met Gln Tyr Gly Thr Val			
450	455	460	
Pro Val Val His Ala Thr Gly Gly Leu Arg Asp Thr Val Glu Asn Phe			
465	470	475	480
Asn Pro Phe Gly Glu Asn Gly Glu Gln Gly Thr Gly Trp Ala Phe Ala			

485

490

495

Pro Leu Thr Thr Glu Asn Met Phe Val Asp Ile Ala Asn Cys Asn Ile
500 505 510

Tyr Ile Gln Gly Thr Gln Val Leu Leu Gly Arg Ala Asn Glu Ala Arg
515 520 525

His Val Lys Arg Leu His Val Gly Pro Cys Arg *
530 535 540

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Oligonucleotide"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GTGGATCCAT GGCGACGCC TCGGCCGTGG

30

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTGAATTCCA TATGGGGCCC CTCCCTGCTC AGCTC

35

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTCTGAGCTC AAGCTTGCTA CTTTCTTC TTAATG

36

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GTCTCCGCGG TGGTGTCTT GCTTCCTAG

29

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGCGTCGCGG AGCTGAGCAG GGAGGTCTCC GCGGTGGTGT CCTTGCTTCC TAG

53

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Cys Val Ala Glu Leu Ser Arg Glu
1 5

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGAGAGAGAG AGAGAG

16

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AAGAAGAAGA AGAAGAAGAA GAAGAAGAAG AAGAAG

36

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AAAAAAAAAAA AAAAAAAA

18

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AGATAATGCA G

11

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

AACAATGGCT

10

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 56 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO..

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Ala Ser Ser Met Leu Ser Ser Ala Ala Val Ala Thr Arg Thr Asn
1 5 10 15

Pro Ala Gln Ala Ser Met Val Ala Pro Phe Thr Gly Leu Lys Ser Ala
20 25 30

Ala Phe Pro Val Ser Arg Lys Gln Asn Leu Asp Ile Thr Ser Ile Ala
35 40 45

Ser Asn Gly Gly Arg Val Gln Cys
50 55

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Ala Pro Thr Val Met Met Ala Ser Ser Ala Thr Ala Thr Arg Thr
1 5 10 15

Asn Pro Ala Gln Ala Ser Ala Val Ala Pro Phe Gln Gly Leu Lys Ser
20 25 30

Thr Ala Ser Leu Pro Val Ala Arg Arg Ser Ser Arg Ser Leu Gly Asn

35

40

45

Val Ala Ser Asn Gly Gly Arg Ile Arg Cys
50 55

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met Ala Gln Ile Leu Ala Pro Ser Thr Gln Trp Gln Met Arg Ile Thr
1 5 10 15

Lys Thr Ser Pro Cys Ala Thr Pro Ile Thr Ser Lys Met Trp Ser Ser
20 25 30

Leu Val Met Lys Gln Thr Lys Lys Val Ala His Ser Ala Lys Phe Arg
35 40 45

Val Met Ala Val Asn Ser Glu Asn Gly Thr
50 55

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Ala Ala Leu Ala Thr Ser Gln Leu Val Ala Thr Arg Ala Gly His
1 5 10 15

Gly Val Pro Asp Ala Ser Thr Phe Arg Arg Gly Ala Ala Gln Gly Leu
20 25 30

Arg Gly Ala Arg Ala Ser Ala Ala Asp Thr Leu Ser Met Arg Thr
35 40 45

Ser Ala Arg Ala Ala Pro Arg His Gln Gln Ala Arg Arg Gly Gly
50 55 60

Arg Phe Pro Phe Pro Ser Leu Val Val Cys
65 70

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Ala Thr Pro Ser Ala Val Gly Ala Ala Cys Leu Leu Leu Ala Arg
1 5 10 15

Xaa Ala Trp Pro Ala Ala Val Gly Asp Arg Ala Arg Pro Arg Arg Leu
20 25 30

Gln Arg Val Leu Arg Arg Arg

35